

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 109507

TO: Karen A Lacourciere Location: CM1/11D0911E12

Art Unit: 1635

Wednesday, December 03, 2003

Case Serial Number: 08765244

From: Barb O'Bryen

Location: Biotech-Chem Library

CM1-6A05

Phone: 308-4291

BOB

barbara.obryen@uspto.gov

Search Notes

RUSH



STIC-Biotech/ChemLib

109507

From: Sent: To: Cc: Subject:	Fredman, Jeffrey Tuesday, December STIC-Biotech/Chem Lacourciere, Karen FW: Rush sequence	r 02, 2003 2:40 PM Lib e search request 08/765,244	
PLEASE RUSI	Н.		
I Approve.			0641
Jeff Fredman			CREV
Original Mess From: Sent: To: Subject:	lage Lacourciere, Karen Tuesday, December 02, 2003 2:08 PM Fredman, Jeffrey Rush sequence search request 08/765,2	144	
Hi Jeff- Could you app biweek and I d Thanks- Karen	rove a RUSH for this search? It is id not realize it had claims to a pai	a short amino acid sequence. ticular sequence.	The case is a 2 month amended due this
Please search Thank-you!	SEQ ID NO:22 in the commercial	databases and pre-grant publ	cations.
Karen A. Lacon CM1 11D09 G (703) 308-75; mailbox 11E12	AU 1635		
Searcher:Phone: Location: Date Picked Up: Date Completed: Searcher Prep/Rev Clerical: Online time:	iew:	TYPE OF SEARCH: NA Sequences: AA Sequences: Structures: Bibliographic: Litigation: Full text: Patent Family: Other:	VENDOR/COST (where applic.) STN: DIALOG: Questel/Orbit: DRLink: Lexis/Nexis: Sequence Sys.: WWW/Internet: Other (specify):

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ALIGNMENTS

RESULT 1

promoter; peptide-nucleic acid; cyclised; gene therapy; target; site-directed mutagenesis; introduction; protein transport. Rat ornithine transcarbamylase signal peptide. AAR90584 standard; Protein; 43 AA. 95DE-1020815. 94DE-4421079. (updated)
(first entry) WPI; 1996-041226/05. Seibel A, Seibel P; (SEIB/) SEIBEL P. DE19520815-A1 16-JUN-1994; 11-JUN-1995; 21-DEC-1995. 25-MAR-2003 31-OCT-1996 Synthetic. AAR90584; AAR90584 HAXAX HAXAX X MX O X MX X B X HAXAX HAXX HAX

Replicable and transcriptionally active plasmid carrying signal peptide for specific target - useful for site directed mutagenesis

us-08-765-244-22.rag

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(TANA/) TANAKA M.
(GIFU-) ZH GIFUKEN KOKUSAI BIO KENYUJO.
(OYOS-) ZH OYO SEIKAGAKU KENKYUSHO.
                                                                                                                          ABG30857 standard; Peptide; 32 AA
                                                                                                                                                                                                    WPI; 2002-569946/61
                                                                                                                                                                JP2002176988-A.
                                                                                                                                                                      25-JUN-2002.
                                                                                    Sequence
                                                                                                                                ABG30857;
                                                                                         Query Match
                                                                                               Matches
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Two modified oligonuclectides (introducing PstI and XhoI sites) were used to amplify a region of the human mitochondrial (mt) genome contg. the light strand promoter, mtDNA ori of the heavy strand, CSB's ("conserved sequence blocks") and a regulation site for DNA replication. Behind this fragment (5' direction) a synthetic multiple cloning site was introduced, generating a product with overhanign ends. The synthetic region also introduced a bidirection) a synthetic fragment and pBluescript sequence. The amplification product, synthetic fragment and pBluescript were ligated and recombinant plasmid 1 (AAT12315) was produced. Human mt is taken to plasmid to form plasmid 2 (AAT12316). The colls and inserted into plasmid to form plasmid 2 (AAT1216). The colls and inserted into plasmid to form plasmid 2 (AAT1216). The colls and insert was isolated as a BsaI fragment and cyclised using hairpin con poligonucleotides, one of which carried the required signal peptide the present sequence. The cyclised product was purified by treatment with exomolease III. In a modification, the signal peptide was attached after cyclisation. The new plasmids were able to impart chloramphenicol resistance to otherwise sensitive B lymphocytes and fibroblasts. Similar plasmids without a signal peptide could not do this. The plasmids can be introduced into eukaryotic cells, site-directed continued as a site-directed continued continued as a site-directed continued con mutagenesis or molecular therapy of genetic diseases, targetting nucleic acid in cells or their organelles via the protein transport route. (Updated on 25-MAR-2003 to correct PR field.) and molecular therapy of genetic diseases Disclosure; Column 11; 24pp; German.

43 AA;

Gaps ; 0 ilarity 100.0%; Score 217; DB 17; Length 43; Conservative 0; Mismatches 0, Thata Indels 1 MLSNIRILLNKAALRKAHTSMVRNFRYGKPVOSQVQLKPRDLC 43 Local Similarity 43;

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(first entry) 07-OCT-2002

Rat ornithine transcarbamylase signal peptide.

peptide; ornithine transcarbamylase; vector; fusion protein; extranuclear Rat; signal recombinant

14-DEC-2000; 2000JP-0380975.

14-DEC-2000; 2000JP-0380975.

N-PSDB; ABK88419

A recombinant vector for expressing a fused protein, useful for decomposing an extranuclear gene of a nonhuman organism -

Disclosure; Page 3; 15pp; Japanese.

ò The invention relates to a recombinant vector for expressing a fused protein containing a fused gene in which a base sequence defining a transfer signal peptide to small cellular organs having an extranuclear gene is combined with a base sequence defining the amino acid sequence a restriction enzyme recognising a defined base sequence. The vector is used for decomposing an extranuclear gene of a nonhuman organism. The present sequence represents the signal peptide of rat mitochondrial ornithine transcarbamylase (MOT) which may be used in the vector of the Gaps . 0 Length 32; Indels . Score 159; DB 23; Pred. No. 2.4e-17; 0; Mismatches 0; 1 MLSNIRILLINKAALRKAHTSMVRNFRYGKPVQ 32 1 MLSNLRILLINKAALRKAHTSMVRNFRYGKPVQ 32 73.3%; Scc... 100.0%; Pre 32; Conservative Query Match Best Local Similarity 32 AA; invention Sequence Matches X88888888888XX ð 원

AAB18445 standard; Protein; 258 AA RESULT 3

15-JAN-2001 (first entry)

Protein encoded by plasmid pUOATP2.

hypotonia; autism; sudden infant death syndrome; hypoglycemia; leukaemia; thrombocytopenia; migraine; hearing loss; stroke; refractory; infantile reflux; carnitine deficiency; multiple sclerosis; blindness; optic atrophy; renal tubular acidosis; cardiomyopathy; chronic pancreatitis; ATPase 6. Leber hereditary optic neuropathy; myoclonic epilepsy; neurogenic muscular weakness; ataxia; retinitis pigmentosa; Kearns-Sayre syndrome; Leigh syndrome; Pearson Marrow pancreas syndrome; aminoglycoside-associated deafness; diabetes; deafness; leukodystrophy; Mitochondrial genome; mitochondrial encephalmyopathy; lactic acidosis;

Synthetic.

WO200053773-A2

14-SEP-2000.

08-MAR-2000; 2000WO-US06037,

99US-0123336, 08-MAR-1999; (USSH) US DEPT HEALTH & HUMAN SERVICES.

Zullo SJ,

WPI; 2000-565602/52. N-PSDB; AAA75084.

or deletions in a mitochondrial genome of a cell, useful for treating diabetes w deafness, comprises introducing mitochondrial DNA into the nuclear Functionally complementing one or more defects, mutations, denome -

Example 1; Fig 3; 49pp; English.

one or more defects, mutations, or deletions in a mitochondrial genome of a cell having a nuclear genome. The method is used for treating a disease or disorder that arises from deletion of the protein-encoding genes of the mitochondrial genome. Alternatively, the method is used for treating a disease or disorder that arises from one or more defects, deletions or The specification describes a method for functionally complementing

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Transcription and translation in the mitochondria. The diseases or disorders that can be ameliorated are mitochondria. The diseases or disorders that can be ameliorated are mitochondrial encephalmyopathy with lactic acidosis and stroke-like episodes, Leber hereditary optic muscular weakness, ataxia, retinitis pigmentosa, Kaarns-Sayre syndrome, muscular weakness, ataxia, retinitis pigmentosa, Kaarns-Sayre syndrome, saintolycomic, mitochondria, Ranns-Sayre syndrome, peatron Marrow pancreas syndrome, aminolycomid-formid, autism with seizures, sudden infant death syndrome with hypoglycemia, leukaemia with maternally inherited thrombocytopenia, migraines (associated with hearing loss, strokes, or diabetes), early harring loss, refractory infantile reflux with optic atrophy and dysolycomia, renal tubular acidosis with elevated lactic acid and hypotonia, nonvalvular hypertrophic cardiomyopathy before age 50 and chronic pancreatitis with stroke-like episodes. The present sequence is encoded by plasmid pUOATP2 comprises a mucant oligomycin-cesistant ATPase 6 mitochondrial gene derived from Chinese hamster ovary (CHO) cells linked to ornithine transcarbamylase DNA sequence. It is used for targeting the protein to the mitochondria.
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  in mitochondrial genes encoding ribosomes or tRNA for
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Pred. No. 2e-08;
2; Mismatches 12; Indels (
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(OYOS-) ZH OYO SEIKAGAKU KENKYUSHO.
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Best Local Similarity
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The present sequence represents the signal peptide of human mitochondrial ornithine transcarbamylase (MOT) which may be used in the vector of the
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68.8%; Pred. No. 2.2e-09;
ive 2; Mismatches 8; Indels
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29-JUL-1994
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                               invention.
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Mitochondrial matrix retention signal

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New vector systems comprise a sequence adapted for intracellular delivery and expression contg. a promoter operably linked to an antibody gene encoding an antibody which binds to a specific target antigen. The antibody is esp. a single chain antibody in which the heavy and light chain variable regions are joined via a hydrophilic linker peptide. Localisation sequences are pref. included in the constructs. The sequence AAR48260 is a mitochondrial matrix retention
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Intracellular binding of antigens - by using antibody targetting with vector system, for e.g. tumour suppression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibody; immune response; modulation; MHC; IRM; receptor; intrabody; major histocompatibility complex; graft rejection; immunomodulatory response molecule; regulation; transplantation;
                                        Single chain antibody; sFv; heavy chain; light chain; variable domain; hydrophilic linker; antibodies; targetting; subcellular localisation signal; mitochondrial matrix; retention signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       retention signal; localisation signal; golgi apparatus; ER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.4%; Score 92; DB 15; Length 32; 61.3%; Pred. No. 6.8e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, Page 103; 155pp; English
                                                                                                                                                                                                                       /note= "not defined"
                                                                                                                                                                  note= "not defined"
                                                                                                                                     Location/Qualifiers
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intracellular binding to a desired target by an intracellularly expressed antibody (i.e. an intrabody) can be used to knock out multiple locuses of immunomodulatory receptor molecules (IRMs), so that the expression of multiple major histocompatibility (MHC) molecules is blocked. This selective targeting of IRMs, their molecules is blocked. This selective targeting of IRMs, their immune system by controlling expression of these molecules and preventing an undesired immune response in a cell. Any component of the MHC pathway or the MHC assembly line or antigen presentation can be targeted. Intrabodies can be used to knock out the immune response in a particular tissue or portion of the body to prepare it for cell or tissue transplantation. Alternatively, an organ for transplantation can be perfused with the intrabody ex vivo. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            intrabodies can comprise whole antibodies, heavy chains, Fab' fragments, single-chain antibodies and diabodies. The intrabodies also comprise an intracellular localisation signal to facilitate interception of expressed proteins. For example, if the target was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a cell surface receptor, the antibody would comprise a leader sequence and an endoplasmic reticulum (ER) or Golgi apparatus retention signal. This peptide is a localisation sequence for the mitochondrial matrix. For other localisation sequences see
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61.3%; Pred. No. 6.8e-07;
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                                                                                                 'note= "Any amino acid"
                                                                                                                                  amino acid"
                                                                                                                                                                  /note= "Any amino acid"
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                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 28; 56pp; English.
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                                                                                                                                'note=
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                                Synthetic
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Regulator; transcription; cell death; phenotype; molecular scaffold; gene therapy; cardiovascular disease; arribthmia; heart failure; ischaemia; obesity; neurodegenerative disease; Alzheimer's disease; bone pathology; dermatologic disease; psoriasis; infection; AIDS; acquired immunodeficiency syndrome; commettic; wound healing; antibiotic transport; drug texicity; drug resistance; immunobilogy; inflammation; allergic response; human immunodeficiency virus. transcriptional regulatory regions, useful for treating cancer, comprises introducing host cells expressing the polypeptide into a library of polynucleotides -Identifying regulator polypeptides which influence target Disclosure, Page 37; 224pp; English. 05-FEB-2001; 2001US-265880P. 27-FEB-2001; 2001US-271423P. 23-JAN-2001; 2001US-26226P. 28-MAR-2000; 2000US-122586P. 04-FEB-2002; 2002WO-US02814, 2001US-265589P. 97US-935377P (UYRP) UNIV ROCHESTER. WPI; 2002-643398/69. WO200262822-A2 Unidentified. 02-FEB-2001; 22-SEP-1997; 15-AUG-2002. Zanderer M,

The invention discloses a method for identifying polymucleotides encoding a regulator polypeptide, whose expression induces activation of a target transcriptional regulatory region in a host cell. The method comprises providing a population of eukaryotic host cells capable of expressing the polypeptides, introducing into the host cells alibrary of polymucleotides and then polypeptides, permitting expression of the polypeptides and then recovering them from the host cells. The target transcriptional regulatory region is operably associated with a polymucleotide encoding a gene product, the expression of which results in host cells dath or cause the host cells to exhibit a pre-determined modified phenotype and where the host cells to exhibit a pre-determined modified phenotype and where the operation of which results of the peptide so that regulatory region. Each candidate regulator polypeptide comprises a candidate peptide and a molecular scaffold fused to the peptide so that the peptide is displayed on the surface of the candidate regulator of polypeptide and a molecular scaffold fused to the peptide so that the peptide is displayed on the surface of the candidate regulator of polypeptide in selections of the regulator molecules, such as polypeptides, which directly or indirectly induce or suppress the transcriptional activation of a target transcriptional regulator regulator molecules may be used (e.g. in gene therapy) for preventing or treating cancers (e.g. breast or ovarian cancer), cardiovascular diseases (e.g. psoriasis), infections (e.g. viral, bacterial), acquired inmunodeficiency syndrome (AIDS), in cosmetic applications and in wound healing. The method is also useful in screening regulator molecules and din improving the performents of existing or resistance applications and in himproving the performent of existing or existance applications and in himproving the performent of existing or processions and in himproving performent of personness and in himproving personness of regulator. The sequences of

Sequence

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42.4%; Score 92; DB 23; Length 32;
llarity 61.3%; Pred. No. 68-07;
Conservative 2; Mismatches 10; Indels
               Local Similarity
les 19; Conserv
Query Match
                     Best Loca
Matches
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1 MLSNIRILLINKAALRKAHTSMVRNFRYGKPV 31
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RESULT 9

ABP56588 standard; Peptide; 32 AA.

ABP56588;

(first entry) 24-MAR-2003

Mitochondrial matrix targeting peptide SEQ ID NO:54.

Identification, intrabody, eukaryotic cell; immunoglobulin; selection, cardiovascular; diminished arrhythmia potential; cardiomyocyte; stroke; enhanced contractile property; heart failure; arrhythmia; embolic; sarcolemmal calcium cycling; arerry, arteriole; angina; atherosclerosis; LDL metabolism; HDL metabolism; skin biology; keloid formation.

Unidentified.

/note= "any amino acid" 'note= "any amino acid" Location/Qualifiers Misc-difference 32 Misc-difference 7 Misc-difference 8

WO200286096-A2.

/note= "any amino acid"

31-OCT-2002.

23-JAN-2002; 2002WO-US01677

23-JAN-2001; 2001US-263225P. 24-JAN-2001; 2001US-263200P. 27-FEB-2001; 2001US-271422P. 15-JUN-2001; 2001US-298095P.

(UYRP) UNIV ROCHESTER MEDICAL CENT.

Zauderer M,

WPI; 2003-103408/09.

Selecting polynucleotides encoding an intracellular immunoglobulin which induces a modified phenotype in a eukaryotic host cell, by introducing library of polynucleotides encoding immunoglobulin subunit polypeptides

Disclosure; Page 44; 257pp; English.

The Property of the property o The present invention describes a method for selecting polynucleotides

therapy for the treatment of disorders such as Alzheimer's disease.

31 AA;

Seguence

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in atherosclerosis-producing mechanisms to find intracellular immunoglobulin molecules that regulate LDL and HDL metabolism; in skin biology applications; and in regulating or inhibiting keloid formation. ABZ22379 to ABZ22449 and ABP56516 to ABP56618 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is a localisation sequence that can be used to direct stabilised single-chain antibodies to the mitochondrial matrix. The N-terminus of the single-chain antibody is linked to a stabilising fusion peptide, referred to as a stabilon, which increases stabilising the antibody against proteolysis in vivo. Degradation of the antibody may be modulated by linking the stabilon to the antibody through a protease-sensitive linker region. The stabilon is removed upon induction of expression of a specific restriction protease by means of an inducible promoter, and this renders the antibody susceptible to proteolysis by the N-end rule pathway. This method for regulating protein stability allows removal of the antibody after it has bound to its target antigen. Stabilised recombinant proteins may be used in gene
and arterioles leading to strokes and angina; in screening for decreases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mitochondrial matrix localisation sequence; single-chain antibody; stabilon; stabilising fusion peptide; vaccine; gene therapy; protein degradation modulation; protein stability; Alzheimer's disease.
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                                                                                                                                                                                                         Gaps
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                                                                                                                                                                 42.4%; Score 92; DB 24; Length 32; larity 61.3%; Pred. No. 6.8e-07; Conservative 2; Mismatches 10; Indels
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(MCIN/) MCINNIS P A.
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                                                                                                                                                                                                                                                                                                                                                                     AAB15704 standard; Peptide; 31
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                                                                                                                                                                                  Similarity
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                                                                                                                                32 AA;
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The invention relates to a controlled release drug delivery system.

Target cells in a patient are transformed with an expression construct encoding an antibody (particularly a single chain antibody) to the drug to be delivered. The antibody contains a modulator of intracellular half-life; this can either be a stabilising or detabilising residue located in the N-terminus after the initial methionine, or a peptide ("stabilon") containing a stabilising residue linked to the antibody N-terminus via a protease cleavage site. On administration of the drug, the antibody binds the drug, localising it at the target cells but maintaining it in an inactive state. As the antibody is degraded (the immescale for which is dependent upon the N-terminal or stabilion amino acids), the drug is released at its site of action where it can exert its effects. The antibody encoded by the expression construct (and characterior the therapeutic agent) can be targetted to particular subcellular localisation signals. The movel method may be used to deliver therapeutic agents to patients with a variety of conditions such as
                                       ij
                                                                                                                                                                                                                                                                                                                                      Controlled release delivery system; drug targetting; drug-specific antibody; intracellular half-life; gene therapy; diabetes; autoimmune disease; inflammatory disease; infectious disease; cancer; side effect; subcellular localisation sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Delivering a drug, to a patient suffering from cancer or diabetes, at a predetermined site, comprises altering a target cell to express a drug specific antibody by gene therapy and administering the drug -
                                       Gaps
                                     1;
   Length 31;
                                   Indels
36.6%; Score 79.5; DB 21;
61.3%; Pred. No. 5.8e-05;
iive 1; Mismatches 10;
                                                                     1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPV 31
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                                                                                                                                                                                                                                                                                                    Mitochondrial matrix localisation signal.
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              diseases and especially cancer. The delivery method of the invention causes a drug to become almost immediately localised at its site of action in an inactive form where it accumulates. Once released by antibody degradation, the drug is at an effective concentration only at the target site, with very little free drug being available in the rest of the body. The system of the invention therefore reduces the side effects caused by therapeutic agents, and also provides economic benefits ABA22837 ABA22837 and ABA22837 represent subcellular localisation the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase; ligase; hyperproliferative disorder; immunodeficiency disorder; autoimmune disorder; entrological disorder; metabolic disorder; inflammatory disorder; cardiovascular disorder; reproductive disorder; blood-related disorder; infectious disorder; cytostatic; anti arthritic; nephrotropic; anticoagulant.
                                                                                                                                                                                                                                                                                                                Gaps
           infectious
                                                                                                                                                                                                                                                                                                                Ή,
                                                                                                                                                                                                                                                                             Length 31;
                                                                                                                                                                                                                                                                                                              Indels
diabetes, autoimmune diseases, inflammatory diseases,
                                                                                                                                                                                                                                                                         36.6%; Score 79.5; DB 21; 61.3%; Pred. No. 5.8e-05;
                                                                                                                                                                                                                                                                                                   10;
                                                                                                                                                                                                                                                                                                                                             1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPV 31
                                                                                                                                                                                                                                                                                                                                                                            MLFNLR-XLINNAAFRHGHNFMVRNFRCGGPL 30
                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human enzyme polypeptide #554.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU23468 standard; Protein; 149 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0179065.
2000US-0180628
2000US-018464.
2000US-01806350.
2000US-0189874.
2000US-0189874.
2000US-0189873.
2000US-0205153.
2000US-0205153.
2000US-0205153.
2000US-0205135.
2000US-0205135.
2000US-0205135.
2000US-0205135.
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2000US-0220963
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                        Local Similarity 61.3
les 19; Conservative
                                                                                                                                                                                                                                      31 AA;
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17-MAR-2000; 2
18-APR-2000; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-MAY-2000;
07-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-FEB-2000;
02-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-DEC-2001
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                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU23468
                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
AAU23468
AAC AAU234
AAC AAU23
AX BAU23
AX BAU33
AX BAU33
AX BAU34
AX BAU34
AX BAU35
AX BAU36
                                                                                                                                                                                                                                                                                                            Matches
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2000US-0226681.
2000US-0226868.
2000US-0227182.
                                                         2000US-0228924.
2000US-0229287.
2000US-0229343.
                                                                                                                                000US-0229509
                                                                                                                                                            2000US-0230437
                                                                                                                                                                           000US-0230438
000US-0231242
                                          :000US-0227009
                                                                                                   000US-0229344
                                                                                                                    000US-0229345
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000US-0233063
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1000US-0236368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               000US-0237038
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2000US-0241787
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3;

Gaps

11; Indels

Length 149;

22;

Score 56.5; D Pred. No. 1.6; 7; Mismatches

40 15;

---KPVQSQVQL-KPR

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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                             N-PSDB; AAS41338
                                            17-NOV-2000;
                                                                                                                                                                                           05-JAN-2001;
                                       17-NOV-2000;
                                                 17-NOV-2000;
17-NOV-2000;
                                                                          17-NOV-2000;
17-NOV-2000;
                                                                                             17-NOV-2000;
17-NOV-2000;
                                                                                                           17-NOV-2000;
17-NOV-2000;
                                                           17-NOV-2000;
                                                                     17-NOV-2000;
                                                                                                                                                             08-DEC-2000;
                                                                                                                                01-DEC-2000;
                                                                                                                                         05-DEC-2000;
                                                                17-NOV-2000;
                                                                                        7-NOV-2000;
                                                                                                                          17-NOV-2000;
                                                                                                       17-NOV-2000;
                                                                                                                      17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                    nvention.
                                                                                                                                                                                                              Rosen CA,
                                                                                                                                                                                                                                                     diseases
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticidaes, therapeutics and pharmaceutical frugs. The invention discloses genomic DNA sequences (ABL/16/76-ABL/30513), expressed DNA sequences (ABL/16/75) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                            LRMTLOKESAMIARSRKPHATMIRNAKYSGLHAGWSLWLPVESALOSHOPR 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 15; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster polypeptide SEQ ID NO 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.9%; Score 54; DB 22; 33.3%; Pred. No. 33; ive 11; Mismatches 7
                                                                                                                                                                    5 LRILLNK-----AALRKAHTSMVRNFRYG--
                                                                                                                                                                                                                                                                                                                   ABB57741 standard; Protein; 866 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PWD,
                                                                                26.0%;
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11-JUL-2000; 2000US-0614150.
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                                                                                                 Best Local Similarity 35.3
Matches 18, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster.
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Matches 15; Conserve
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                                          149 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      866 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pharmaceutical
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                                                                                                                                                                                                                                                                                                                                                                                                       26-MAR-2002
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                                        Sequence
                                                                                Query Match
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                                                                                                                                                                                                                                                                        RESULT 1
ABB57741
                 XX SS
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                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                       Purlypeprings, and the purpose of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyasses, functional classes of oxidoreductases, transferases, hydrolases, lyasses, disomerases or ligases. The sequences of the invention are useful in the disomerases or ligases. The sequences of the invention are useful in the disonders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. AIDS) autoimmune disorders
(e.g. arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic disorders (e.g. phraylketonuria), inflammatory disorders
(e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), blod-related disorders (e.g. hemophilia), reproductive disorders
(e.g. infertility) and infectious disorders (e.g. Influenca). The polynucleotides of the invention can also be used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to the isolation of novel human enzyme polypeptides, and the CDNA (AAS40785-AAS41684) and genomic sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11; SEQ ID No 1464; 1180pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barash SC, Ruben SM;
08-NOV-2000; 2000US-0246527.

08-NOV-2000; 2000US-0246528.

08-NOV-2000; 2000US-0246532.

08-NOV-2000; 2000US-0246609.

08-NOV-2000; 2000US-0246610.

08-NOV-2000; 2000US-0246611.

08-NOV-2000; 2000US-0246611.
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2000US-0249297.
2000US-0249299.
2000US-0249300.
2000US-0250301.
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2000US-0249209.
2000US-0249210.
2000US-0249210.
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2000US-0249216.
2000US-0249217.
2000US-0249217.
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2000US-0249245.
2000US-0249264.
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2000US-0251988.
2000US-0256719.
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2000US-0249213
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2000US-0251856
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Myers EW;

<u>س</u>

Gaps

12;

7; Indels

41

RESULT 14

2 LSNLRILLNKAALRKAHTSMVRNF-RYGK----PVQSQVQLKPRD

à g

Length 866;

Goguet de la Salmoniere Y;

Portnoi D,

Pelicic V,

98WO-FR01813. 97FR-0011325. 97FR-0010404.

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proteins from various Mycobacterium species microorganisms. The encoding nucleotide sequences can be used as primers and probes for methods for detecting and identifying mycobacteria, especially belonging to the M. tuberculosis complex. The encoded proteins can be used in vaccines for immunisation against a bacterial or viral infection.
                                                                                                                                                                                                                                                                                                                                                                 Sequences AAY04742-Y05000 and AAY07201-Y07204 represent secreted
                                                                                                                                                                                                                                                                        Mycobacterial DNA vectors containing reporter constructs - for identifying coding or promoter sequences involved in infection-associated protein expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |::| | |||: | | |||
119 RVILRCAHTRKANQSRARTLRPLRPL--RIALRPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 RILLNKAALRKAHTSMVRNFRYGKPVQSQVQLKPR
                                                                                                                                                                                                                                                                                                                                       Claim 32; Fig 38B; 309pp; French.
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1 Similarity 37.1%;
13; Conservative
                                                                                                                                                       (INSP ) INST PASTEUR
                                                                                                                                                                                                                               WPI; 1999-181045/15.
N-PSDB; AAX34186.
                                                                                                                                                                                     Lim EM,
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            165 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: Job time : 42 secs
                    WO9909186-A2
                                                                               14-AUG-1998;
                                                                                                             11-SEP-1997;
                                                                                                                           14-AUG-1997;
                                                                                                                                                                                   Gicquel B,
Guigueno A;
                                                  25-FEB-1999
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Matches
    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLO18A-ABL30511), expressed DNA sequences (ABLO18A-ABL30511), appressed DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ABBS/737-ABB/2072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                    Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 4569; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 22; Length 755;
                                                                                                        Drosophila melanogaster polypeptide SEQ ID NO 4569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.7%; Score 53.5; D
42.5%; Pred. No. 33;
:ive 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 Myers EW;
               ABB59259 standard; Protein; 755 AA.
                                                                                                                                                                                                                                                                                                                                                                               PWD,
                                                                                                                                                                                                                                                                        23-MAR-2001; 2001WO-US09231.
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                              Adams M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            755 AA;
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N-PSDB; ABL03362
                                                                                                                                                                                                              WO200171042-A2
                                                                                                                                                    pharmaceutical
                                                                                                                                                                                                                                            27-SEP-2001
                                              ABB59259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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ABB59259
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completed: December 3, 2003, 14:32:33
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<u>ب</u>

Gaps

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Indels

15;

Conservative

Local Similarity tes 17; Conserv

Best Loc Matches

2 LSNLRILLINKAALRKAHTSMVRNFRYGKPVQSQVQLKPRD 41

g à

Secreted protein; Mycobacterium; primer; PCR; amplification; probe; hybridisation; detection; vaccine; immunisation; infection.

Mycobacterium sp

Mycobacterium species protein sequence 38B

(first entry)

06-JUL-1999

AAY04933;

AAY04933 standard; Protein; 165 AA

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Gaps

7

12;

Score 52; DB 20; Pred. No. 8.9; 8; Mismatches 12

151 40

Length 165; Indels

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LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLLGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRAGMENT TYPE: N-terminal ORIGINAL SOURCE: US-08-373-190-29
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2, Appli
2, Appli
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5399, Ap
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Sequence 18053, A
Sequence 2, Appli
                                                                                           ; Search time 22 Seconds (without alignments) 82.698 Million cell updates/sec
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Sequence 1, Ag
Sequence 3, Ag
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Sequence 29,
Sequence 29,
Sequence 42,
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Sequence 29
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Sequence 1
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Sequence 2
Sequence 5
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Sequence 1
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217
1 MLSNLRILLINKAALRKAHTS......NFRYGKPVQSQVQLKPRDLC
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/cgm2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgm2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgm2_6/ptodata/1/iaa/6G_COMB.pep:*
/cgm2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgm2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-215-29
US-09-287-145A-29
US-09-556-111-29
US-09-413-814-42
US-09-4252-991A-18053
US-09-252-991A-18053
US-08-542-921-2
US-08-542-921-2
US-08-685-2
US-08-107-532A-5399
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US-09-252-991A-18693
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                                                                                                                                                                                                                                                                           328717 segs, 42310858 residues
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                                                                                           December 3, 2003, 14:31:47
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Maximum Match 100%
Listing first 45 summaries
                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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Sequence 10, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 2355, Appl Sequence 27, Appl Sequence 14, Appl Sequence 110, Appl Sequence 10, Appl Sequence 10, Appl Sequence 5, Appli Sequence 6926, Appli Sequence 6926, Appli Sequence 6926, Appli Sequence 6926, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 6926, Appli Appli Sequence 6926, Appli		BINDING OF PROTEINS
US-08-582-776C-10 US-08-434-831B-10 US-08-313-553-15 US-08-767-991A-32535 US-09-255-991A-32535 US-09-285-858-27 US-09-255-991A-28901 US-09-255-991A-28901 US-09-312-762A-14 US-09-107-532A-5110 US-09-107-532A-5110 US-09-107-532A-5110 US-09-107-532A-5110 US-09-107-532A-5110 US-09-107-532A-5110 US-09-107-532A-5110 US-09-107-532A-5110 US-09-108-989-5 US-09-255-991A-26810 US-09-252-991A-26810	ALIGNMENTS	INTRACELLULAR ROBERTS & CUSE 3,190 66735 56-PCT-US
21.2 21.2 21.2 21.2 21.2 21.2 21.2 21.2 21.2 21.2 21.2 21.2 21.2 21.2 22.7 22.7 23.6 4 4 4 20.7 23.6 4 4 20.7 23.6 4 4 20.7 23.6 4 4 60.9 4 60.9 4 60.9 7 60.9 4 60.7 7 60.9 7 60.9 7 60.9 7 60.9 7 60.9 7 60.9 7 60.9 7 60.9 7 60.9 7 60.9 7 60.9 7 60.9 7 60.9 7 60.9 7 60.9 7 60.9 80.7 7 80.7 7 80.7 7 80.7		T. 1 1-373-190-29 PURDLE 29, Application US/08373190 PURDLE CANT. BARASCO, WAYNE APPLICANT: HARELITURN, WILLIAM TITLE OF INVENTION: METHOD OF INVENTION: HARELITURN, WILLIAM TITLE OF INVENTION: METHOD OF INVENTION: METHOD OF INVENTION: TO STREET: 130 WATER STREET COMPUTER: BOSTON STRATE: MA COUNTRY: US ZIP: 02.109 COMPUTER READBLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM COMPATIBLE OPERATING SYSTEM: US/08/373, FILING DATE: 17-JAN-1995 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/373, FILING DATE: 16-JUL-1993 ATTORNEY, AGENT INPORMATION: NAME: RESULCATION NUMBER: 34,235 REGISTRATION NUMBER: 34,235 REFERENCE/DOCKET NUMBER: 34,235 REFERENCE/DOCKET NUMBER: 34,235 REFERENCE/DOCKET NUMBER: 34,235 REFERENCE/DOCKET NUMBER: 31,235 TELEPHONE: 617-523-3440 TELEPHONE: 617-523-3440 TELEPHONE: STRE UR 2002 FORMATION POR SEQ ID NO: 29: FURNISH STREETERING NUMBER: STRE UR 2002 TELEPHONE: GLOSSEN LENGTHERISTICS: LENGTHER STREETERING NUMBER: STREETER TENDER SEQ ID NO: 29: EDEMORIAL STREETER TENDER SEG ID NO: 2002 FORMATION POR SEG ID NO: 2003
8 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		RESULT 1 US-08-373-190-29 Sequence 29, Application US/083731 Sequence 29, Application US/083731 GENERAL INFORMATION: APPLICANT: MAZASCO, WAXNE TITLE OF INVENTION: METHOD OF NUMBER OF SEQUENCES: 79 CORRESPONDENCE BADRESS: ADDRESSEE: DIKE, BRONSTEIN, STREET: 130 WATER STREET CITY: BOSTON STREET: MA COUNTRY: US ZIP: 02109 COMPUTER READABLE FORM: MEDIUM TYPE: DISKette COMPUTER: IBM COMPATIBLE COMPUTER: IBM COMPATIBLE OMPUTER: READABLE FORM: MEDIUM TYPE: DISKET COMPUTER: IBM COMPATIBLE OMPUTER: STREET OMPUTER: IBM COMPATIBLE OMPUTER: IBM COMPATIBLE OMPUTER: IBM COMPATIBLE OMPUTER: STREET OMPUTER: STREET OMPUTER: IBM COMPATIBLE OMPUTER: STREET OMPUTER: STREET OMPUTER: IBM COMPATION: IBM COMPATION: TELEFPANCE CHARACTERISTICS: IBM COMPATIBLE CHARACTERISTICS
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DB 2; Length 32;

42.4%; Score 92;

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/287,145A
FILING DATE:
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APPLICATION NUMBER: US/08/438,190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 29, Application US/09287145A Patent No. 6072036 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: EISENSTEIN, RONALD I.
REGISTRATION NUMBER: 30628
REPERENCE/DOCKET NUMBER: 41956
TELECOMUNICATION IRPORMATION:
TELEPHONE: (617) 523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 130 WAIER STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: US
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                                            MASSACHUSETTS: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
US-08-350-215-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-287-145A-29
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Patent No. 6004940
GENERAL INFORMATION:
APPLICANT: MARASCO, WAYNE A.
APPLICANT: RICHARDSON, JENNIFER
TITLE OF INVENTION: INTRACELLULAR TARGETING OF ENDOGENOUS
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 58
                                                                                                                                                                                                                                                                                                                                              Sequence 29, Application US/08438190A
Patent No. 5965371
GENERAL INFORMATION:
APPLICANT: MARASCO, WAYNE
APPLICANT: HASELTINE, WILLIAM
TITLE OF INVENTION: METHOD OF INTRACELLULAR BINDING OF
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN, DIKE, BRONSTEIN, ROBERTS & ADDRESSEE: CUSHMAN
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ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & ADDRESSEE: CUSHMAN
                                            Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,190A
   Pred. No. 9.2e-08;
2; Mismatches 10
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61.3%; Pred. No. 9.2e-08;
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FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: EISENSTEIN; RONALD I.
REGISTRATION NUMBER: 30628
REFERENCE/DOCKET NUMBER: 41956
TELEPHONE: (617) 523-6440
TELEPAX: (617) 523-6440
TELEFAX: (617) 523-6440
TELEFAX: (617) 523-6440
TELEFAX: (617) 523-6440
TELEFAX: (617) 523-6410
TELEFAX: (617) 523-6440
TELEFAX: (617) 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
61.3%;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 61.3
Matches 19; Conservative
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Best Local Similarity 61.3
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: BOSTON
STATE: MASSACHUSETTE
COUNTRY: US
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GY: linear
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TOPOLOGY:
US-08-438-190A-29
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US-08-438-190A-29
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US-08-350-215-29
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APPLICANT: MARSCO, WAYNE
APPLICANT: MASELTINE, WILLIAM
TITLE OF INVENTION: METHOD OF INTRACELLULAR BINDING OF
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 32;
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,215
FILING DATE: 12-DEC-1994
CLASSIFICATION S14
ATTORNEY/AGENT INFORMATION:
NAME: BISENSTEIN, RONALD I.
RESIFICATION NUMBER: 30628
REFERENCE/DOCKET NUMBER: 41956-CP3
TELEPHONE: (617) 523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25
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42.4%; Score 92; DB 3;
Best Local Similarity 61.3%; Pred. No. 9.2e-08;
Matches 19; Conservative 2; Mismatches 10
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APPLICANT: Mueller, Joachim
APPLICANT: Mueller, Joachim
APPLICANT: Reichenbach, Hans
TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
TITLE OF INVENTION: DATE: 1999/23535
CURRENT APPLICATION NUMBER: US/09/413,814
EARLIER APPLICATION NUMBER: US 1994/43,814
EARLIER FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 42
                                                    Sequence 42, Application US/09413814
Patent No. 6225064
GENERAL INFORMATION
APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH
APPLICANT: Bristol-Myers Squibb, Co.
APPLICANT: Beyer, Stefan
APPLICANT: Bloeck, Helmut
APPLICANT: Bloeck, Helmut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Sorangium cellulosum
                                                                                                                                                                                                                                           APPLICANT: Cino, Paul M
APPLICANT: Dougherty, Brian A
APPLICANT: Goldberg, Steven I
APPLICANT: Hofle, Gerhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 35.5
Matches 11; Conservative
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ADDRESSEE: DAVID G. CONLIN, DIKE, BRONSTEIN, ROBERTS
CUSHMAN
                                                                                                                                                                                                                   Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42.4%; Score 92; DB 4; Length 32; 61.3%; Pred. No. 9.2e-08; ive 2; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: MARASCO, WAYNE
HASELTINE, WILLIAM
TITLE OF INVENTION: BETHOD OF INTRACELLULAR BINDING
PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                            42.4%; Score 92; DB 3; 51.3%; Pred. No. 9.2e-08; tive 2; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/556,111
FILING DATE: 21-Apr-2000
CLASSIFICATION: Unknown>
PRIOR APPLICATION DATA:

APPLICATION DATA:
APPLICATION NUMBER: 08/438,190
FILING DATE: CURKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: EISENSTEIN, RONALD I.
REGISTRATION NUMBER: 30628
REFERENCE/DOCKET NUMBER: 41956
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
                                                                                                                                                                                                                                                                                                                                                 1 MLFNLRXXLNNAAFRHGHNFMVRNFRCGQPL 31
                                                                                                                                                                                                                                                                                                     1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPV 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE DESCRIPTION: SEQ ID NO: 29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 29, Application US/09556111 Patent No. 6329173 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 130 WATER STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02109
COMPUTER READABLE FORM:
  (617) 523-6440
              TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
                                                                                                                                                                                                          Query Match
Best Local Similarity 61.3
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: US
                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                              US-09-287-145A-29
                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
US-09-556-111-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-556-111-29
TELEFAX:
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Gaps

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Indels

8; Mismatches

Length 2539;

DB 3;

Score 54; Pred. No.

35.5%;

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Sequence 32812, Application US/09252991A

Patent No. 6521795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS.
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT PILION NUMBER: US/09/252,991A
CURRENT PILION DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PAPLICATION NUMBER: US 60/074,788
PRIOR PELICATION NUMBER: US 60/094,190
PRIOR PELICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 32812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (451)
OTHER INFORMATION: Identity of amino acid at the above locations are unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15;
                       |:|:||:||:|
1969 ASLKSAHSSEPEPARHGRPALSSEWVAPRNV 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 ILLNKAALRKAHTSMVRNFRYGKPVQSQVQLK 38
12 AALRKAHTSMVRNFRYGKPVQSQVQLKPRDL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.4%; Score 53; DB 34.4%; Pred. No. 4.1; ive 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                             RESULT 7
US-09-252-991A-32812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-252-991A-32812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 457
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Gaps

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10; Indels

Conservative

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359 LSNLQILVNYQINGSAWRGSRVRYHYLHSSIIQEKSYGLLSDPVGANINVQNNDI 413
                                                                                                                                                                                                                                                                                                                                                                                                                   ---KAALRKAHTSMVRNFRYG---KPVQSQVQLKPRDL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---KAALRKAHTSMVRNFRYG---KPVOSOVQLKPRDL 42
                                                                                                                                                                                                                                                                          23.5%; Score 51; DB 1; Length 1169; 25.5%; Pred. No. 28; tive 12; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.5%; Score 51; DB 2; Length 1169; 25.5%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: IIZUKA, TOSHIHIKO
APPLICANT: TAGAWA, MICHITO
APPLICANT: TAGAWA, MICHITO
APPLICANT: ARAI, SATOSHI
APPLICANT: NIIZEKI, MASATSUGU
APPLICANT: NIYAKE, TOSHIKO
TITLE OF INVENTION: NOVEL BACILLUS STRAIN AND HARMFUL
TITLE OF INVENTION: ORGANISM CONTROLLING AGENTS
TOWERSPONDENCES:
CORRESPONDENCES:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDITUM TYPE: Floppy disk
COMPUTER: EM P. Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURSENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,685
FILING DATE: 23-JUN-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/542,921
FILING DATE: 13-OCT-1995
APPLICATION NUMBER: US 276082/94
FILING DATE: 14-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAMME: OBLON, NORMAN F
REGISTRATION NUMBER: 49-209-0
TELECOMMUNICATION NUMBER: 49-209-0
TELECOMMUNICATION NUMBER: 49-209-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08880685
Patent No. 5834296
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (703) 413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 1169 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFRANE: (703) 413-300
TELEFRA: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2
                                SEQUENCE CHARACTERISTICS:
LENGTH: 1169 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 25.5
Matches 14, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 25.5
Matches 14; Conservative
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
LENGTH: 1169 amino aci
                                                                                                                      ; TOPOLOGY: linear;
; MOLECULE TYPE: protein
US-08-542-921-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein US-08-880-685-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 LSNLRILLN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                   2 LSNLRILLN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-880-685-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
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                                                                                                               Sequence 18053, Application US/09252991A

Batent No. 6551795
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
SEQ ID NOS: 33142
SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ξ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MLSNLRILLNKAALRK-----AHTSMVRNFRYGKPVQSQVQLKPRDL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 52; DB 4; Length 218;
Pred. No. 2.4;
6; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSES: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ARAI, SATOSHI
APPLICANT: NIZEKY, MASATSUGU
APPLICANT: NIZEKY, MASATSUGU
APPLICANT: NIYAKE, TOSHIRO
TITLE OF INVENTION: NOVEL BACILLUS STRAIN AND HARMFUL
TITLE OF INVENTION: ORGANISM CONTROLLING AGENTS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONTINUED IN THE STATEM TO SOFTWARE SOFTWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-542-921-2
Sequence 2, Application US/08542921
Patent No. 5736514
GENERAL INFORMATION:
APPLICANT: IIZUKA, TOSHIHIKO
APPLICANT: TAGAWA, MICHITO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.0%;
ilarity 33.3%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                             -09-252-991A-18053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
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APPLICAMT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBNCE: 107196,136
CURRENT FILING DATE: 1999-02-18
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
RIOR APPLICATION NUMBER: US 60/094,190
RRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 18693
LENGTH: 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22.8%; Score 49.5; DB 4; Length 523; 25.5%; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4;
                                                                                                                                                                                                                             SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/05/51
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22.8%; Score 49.5; Dilarity 40.7%; Pred. No. 5.6; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAMB/KEY: misc_feature

LOCATION: (B) LOCATION 1...208

SEQUENCE DESCRIPTION: SEQ ID NO: 5399:
US-09-107-532A-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 NKAALRKAHTSMVRNFRYGKPVQSQVQ 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18693, Application US/09252991A Patent No. 6551795
GENERAL INFORMATION
APPLICANT: Marc J. Rubenfield et al
                                                                                                        ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                   COMPUTER: PC
OPERATING SYSTEM: <Unknown>
              STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 208 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 5399
SEQUENCE CHARACTERISTICS:
                                                              STATE: Massachusetts
                                          CITY: Waltham
                                                                                       COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
US-09-252-991A-18693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-252-991A-18693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCCCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7
359 LSNLQILVNYQTNGSAWRGSRVRYHYLHSSIIQEKSYGLLSDPVGANINVQNNDI 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --KAALRKAHTSMVRNFRYG---KPVQSQVQLKPRDL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23.5%; Score 51; DB 2; Length 1169; 25.5%; Pred. No. 28; ive 12; Mismatches 15; Indels
                                                                                                                                 GENERAL INFORMATION:
APPLICANT: 1IZUKA, TOSHIHIKO
APPLICANT: ARAI, SATOSHI
APPLICANT: MACHITO
APPLICANT: MACHITO
APPLICANT: MACHITO
APPLICANT: MIZEKI, MACHITO
APPLICANT: MIZEKI, MACHITO
TITLE OF INVENTION: NOVEL BACILLUS STRAIN AND HARMFUL
TITLE OF INVENTION: ORGANISM CONTROLLING AGENTS
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCIFILAND
                                                                                                                                                                                                                                                                                                                                                                                                              E: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,684
FILING DATE: 23-JUN-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/542,921
FILING DATE: 13-0CT-1995
APPLICATION NUMBER: UP 276082/94
FILING DATE: 14-0CT-1994
ATTORNEY/AGENT INFORMATION:
NAMME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFIERRICE/DOCKET NUMBER: 49-209-0
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: 49-209-0
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
SEGUENCE CHARACTERISTICS:
LENGTH: 1169 amino acids
TTYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5399, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                          Sequence 2, Application US/08880684
Patent No. 5837526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 25.5
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-880-684-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-107-532A-5399
                                                                                              US-08-880-684-2
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US-09-950-046A-2
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Job time
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     Gaps
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     15;
                                                                                                                                                                                                     APPLICANT: Kwiatkwwski, David J.
APPLICANT: Sampson, Julian R.
APPLICANT: Povey, Sue
APPLICANT: van Slegtenhorst, Marjon
APPLICANT: Halley, Dicky
TITLE OF INVENTION: Compositions and Methods Based U
TITLE OF INVENTION: Sclerosis-1 (TSC-1) Gene and Gene Product
CORRESPONDENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Vinson & Elkins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
                                                         DB 4; Length 1164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --GKPVOSQVQLK 38
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     9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPUTER: OPERATING SYSTEM: PC-DOS/MS-DOS COFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWAKE: FACTOR DATA:

APPLICATION DATA:

TILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sanzo, Michael A.
REGISTRATION NUMBER: 36,912
REFERENCE/DOCKET NUMBER: BRI31/42002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 639-6685
TELEPAK: (202) 639-664
INFORMATION FOR SED ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1164 amino acids
   11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 49.5; D
Pred. No. 48;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                1455 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kwiatkowski, David J. Sampson, Julian R. Povey, Sue van Slegtenhorst, Marjon Halley, Dicky
                                                                                                                                                                                                                                                                                                                                                                                                                STAIR.
COUNTRY.
1.S.
ZIP: 2004-1008
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
TYPE: Floppy disk
PC Compatible
PC PC POSS/MS-D/
PC-DOS/MS-D/
PC-DOS/MS-D/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09950046A Patent No. 6548258 GENERAL INFORMATION:
                                                                                                                                                     Sequence 2, Application US/09457708
Patent No. 6326483
                                   6 RILLNKAALRKAHTSMVRNFRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3S: not relevant
not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 22.8%;
Best Local Similarity 29.8%;
Matches 14; Conservative
12; Conservative
                                                                                                                                                                                                                                                                                                                                                                       STREET: 1450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Kwiatk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino ac
STRANDEDNESS:
TOPOLOGY: not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ANTI-SENSE: NO
US-09-457-708-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
US-09-950-046A-2
                                                                                                                    RESULT 14
US-09-457-708-2
Matches
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TITLE OF INVENTION: Compositions and Methods Based Upon the Tuberous Sclerosis-1 (TSC-1) Gene and Gene Product
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 1164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  806 MIABLRIELKKANNKVCHTBLLLSQVSQKLSNSESVQQQMEFLNRQL 852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                   COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/950,046A
FILING DATE: 12-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MLSNLRILLNKAALRKAHTSMV----RNFRYGKPVQSQVQLKPRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19;
                                       NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSE: Vinson & Elkins
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Sanzo, Michael A.
REGISTRATION NUMBER: 36,912
REFERENCE/DOCKET NUMBER: BRI331/42002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 49.5; DB
Pred. No. 48;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3, 2003, 14:34:53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AMTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 639-6585
TELEFAX: (202) 639-6604
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1164 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.8%;
29.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14; Conservative
                                                                                                                                                                          COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       completed: December
He : 23 secs
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Matches 14; Conserv
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December 3, 2003, 14:32:37; Search time 30 Seconds (without alignments) 266.577 Million cell updates/sec
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1 MLSNIRILLINKAALRKAHTS......NFRYGKFVQSQVQLKPRDLC 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*

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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW PUB.pep:*

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10: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US08_NEW PUB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US08_NEW PUB.pep:*

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16: /cgn2_6/ptodata/1/pubpaa/US106_PUBCOMB.pep:*

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17: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*

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17: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                684280 seqs, 185983659 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0 Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                         US-08-765-244-22
                                                                                                                                                                                                                                                                                                                                                                 Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database :
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Segmence 22. Appl	Sequence 1. Appli	Segmence 48. April	Segmence 54 Appl		`~	, α	Semience 7915 An	Segmence 7102 An	Segment 2 annuli	Semience 46024 a	Semience 4869 An	Segretary 1000	Section 2017	Somionee 3822, Ap	aednemce 4120, Ap
SUMMARIES	£		US-08-765-244-22	US-08-765-244-1	US-10-061-395-48	US-10-052-942-54	US-09-998-027-3	US-10-165-099-3	US-10-353-856-8	US-10-156-761-7915	US-10-032-585-7102	US-09-950-046A-2	US-09-864-761-46024	US-09-815-242-4869	US-09-815-242-10798	US-09-738-626-305	173-09-764-891-4156	0014 100 100 00
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	Query Match Length DB		43	41	32	32	1286	1286	2212	414	564	1164	75	285	334	684	235	
%	Query		100.0	8.06	42.4	42.4	28.1	28.1	23.3	23.0	23.0	22.8	22.4	22.4	22.4	22.4	22.1	
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	, Appli	3. Appli	518. An	1. Appl	Annli	Appli	App.	B. Arn	57. Ann	904. 4	7. App	A. Appl	7. Appl	7. Appl	7. Appl	Ann]	Z. App.	7 200	1993. A	Appli	LO. App	Appl	Appl	Appl	Appl	Appl	Appl	Appli	35. App	54, App
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Č	-10-061-201	-201	-585	-247	-627	-627	-962	-608	-685	761-	284-	-293	-875	-878	-786	-710	-859	-846	-761	-026	-752	-067	-762	-078	-977	-774	-352	-279	59-730-1	-639
	-061	-061	1-032	-756	1-357	-357	-211	-080	-370	864-	811-	-177	-270	-270	-270	-270	-270	-270	-156	-147	-881	-988	-312	-015	-238	-114	-099	-074	-969	-774
1	OS-10	US-10	US-10	0S-05	US-10	US-10	US-10	US-10	US-10	9 US-09-864-761-35904	US-09-	US-10	US-10	US-10	US-10	US-10	US-10	US-10	US-10	US-10	US-09	US-09	US-09	0S-09	US-10	US-10	US-10	US-10	US-09	US-09
•	77	12	12	12	12	12	15	12	12	9	9	72	15	15	15	15	15													
Ç	9 7 9	729	1987	826	421	421	629	1139	1139	1551	187	513	761	761	761	761	761	761	808	920	511	511	535	700	700	716	730	459	103	104
,	7.77	22.1	22.1	21.9	21.7	21.7	21.4	21.2	21.2	21.2	21.0	21.0	21.0	21.0	21.0	21.0	21.0	21.0	21.0	21.0	20.7	20.7	20.7	20.7	20.7	20.7	20.7	20.5	20.3	20.3
0	40	48	48	47.5	47	₹#	46.5	46	46	46	45.5	45.5	45.5	45.5	45.5	45.5	45.5	45.5	45.5	45.5	45	45	45	45	45	45	45	44.5	44	44
Ų	D I	17	18	13	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	32	36	37	38	33	40	41	42	43	44	45

ALIGNMENTS

JS-08-765-244-22

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JOHNSTON LINCOLD AND THE APPLICANT: Seibel, Peter

APPLICANT: Seibel, Andrea

APPLICANT: Seibel, Andrea

TITLE OF INVENTION: FRAGMENT, PROCESS FOR PRODUCING THE SAME AND ITS USES FOR

TITLE OF INVENTION: APPROPRIATELY INTRODUCING THE SAME AND ITS USES FOR

TITLE OF INVENTION: APPROPRIATELY INTRODUCING THE SAME AND ITS USES FOR

TITLE OF INVENTION: APPROPRIATELY INTRODUCING THE SAME AND ITS USES FOR

TITLE OF INVENTION: APPROPRIATELY INTRODUCING THE SAME AND ITS USES FOR

TITLE OF INVENTION: APPROPRIATE 1999-

CURRENT APPLICATION NUMBER: US/08/765,244

TRICK APPLICATION NUMBER: DE 44 21 079.5

PRIOR FILING DATE: 1994-06-16

NUMBER OF SEQ ID NOS: 22

SEQ ID NOS: 22

SEQ ID NOS: 22

TOWNSHIP PRICK APPLICATION NUMBER: PARISEQ FOR WINDOWS Version 4.0
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100.0%; Score 217; DB 8; Length 43;
Best Local Similarity 100.0%; Pred. No. 4e-25;
Matches 43; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MLSNLRILLINKAALRKAHTSMVRNFRYGKPVQSQVQLKPRDLC 43
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Sequence 22, Application US/08765244
Publication No. US20010008771A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Rattus rattus
US-08-765-244-22
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RESULT 2 US-08-765-244-1 ; Sequence 1, Application US/08765244

US20010008771A1

Publication No.

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APPLICANT: Smith, Ernest
APPLICANT: Smith, Ernest
APPLICANT: Wei, Chungwen
TILE OF INVENTION: Methods of Producing or Identifying Intrabodies in Bukaryotic C.
FILE REFERENCE: 1821.0090004
CURRENT FILING DATE: 2002-01-23
PRIOR APPLICATION NUMBER: 60/298,095
PRIOR APPLICATION NUMBER: 60/298,095
PRIOR APPLICATION NUMBER: 60/271,422
PRIOR APPLICATION NUMBER: 60/271,422
PRIOR APPLICATION NUMBER: 60/263,200
PRIOR APPLICATION NUMBER: 60/263,200
PRIOR FILING DATE: 2001-01-24
PRIOR PILING DATE: 2001-01-24
PRIOR FILING DATE: 2001-01-23
NUMBER OF SEQ ID NOS: 154
SOFTWARE: Patentin version 3.0
SEQ ID NO 54
LENGTH: 32
MUNDER OF SEQ ID NOS: 154
LENGTH: 32
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Publication No. US20030093819A1
GENERAL INFORMATION:
APPLICANT: D'Andrea et al.
TITLE OF INVENTION: Methods and Compositions for the
TITLE OF INVENTION: Diagnosis and Treatment of Cancers Associated with Defective
FILE REFERENCE: 2486/101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TEATURE:

OTHER INFORMATION: signal sequence
NAME/KEY: UNBURE

LOCATION: (7)..(8)

OTHER INFORMATION: Xaa may represent any amino acid
LOCATION: (32)..(32)

OTHER INFORMATION: Xaa may represent any amino acid
COTHER INFORMATION: Xaa may represent any amino acid
US-10-052-942-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42.4%; Score 92; DB 15;
61.3%; Pred. No. 1.3e-06;
cive 2; Mismatches 10
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CURRENT FILING DATE: 2001-11-02
NUMBER OF SEQ ID NOS: 191
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1286
                                                                                    Sequence 54, Application US/10052942
Publication No. US20030104402A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (1)...(1286)
; OTHER INFORMATION: Plantfancd2
US-09-998-027-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                              APPLICANT: Zauderer, Maurice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 61.3
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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NAME/KEY: PEPTIDE
                                                          -10-052-942-54
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APPLICANT: Seibel, Peter
APPLICANT: Seibel, Andrea
TITLE OF INVENTION: CHIMERICAL PEPTIDE-NUCLEIC ACID
TITLE OF INVENTION: FRAGMENT, PROCESS FOR PRODUCING THE SAME AND ITS USES FOR
TITLE OF INVENTION: AND CELLS
TITLE OF INVENTION AND CELLS
TITLE OF INVENTION: APPROPRIATELY INTRODUCING NUCLEIC ACIDS INTO CELL ORGANELLES
TITLE OF INVENTION: AND CELLS
TITLE OF INVENTION: AND CELLS
TITLE OF INVENTION: AND CELLS
TITLE OF INVENTION NUMBER: US/08/765,244
CURRENT APPLICATION NUMBER: DCT/DE95/00775
PRIOR APPLICATION NUMBER: DCT/DE95/00775
PRIOR APPLICATION NUMBER: DCT/DE95/00775
PRIOR PILLING DATE: 1994-06-16
NUMBER OF SEQ ID NOS: 22
SOFFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 41
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OTHER INFORMATION: Heterologous signal sequence for the mitochondrial matrix
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US-10-61-395-48

i Sequence 46, Application US/10061395

i Publication No. US20020192675A1

GENERAL INFORMATION:
APPLICANT: Zauderer, Maurice
APPLICANT: Smith, Ernest S.
TITLE OF INVENTION: Methods of Identifying Regulator Molecules
FILE REPRENCE: 1221.0080003
CURRENT APPLICATION NUMBER: US/10/061,395
CURRENT FILING DATE: 2002-02-04
FRIOR PRIOR FILING DATE: 2001-02-07
FRIOR FILING DATE: 2001-02-07
FRIOR FILING DATE: 2001-02-05
FRIOR PRIOR FILING DATE: 2001-02-05
FRIOR PRIOR FILING DATE: 2001-02-05
FRIOR FILING DATE: 2001-02-05
FRIOR FILING DATE: 2001-02-05
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FRIOR PRIOR FILING DATE: 2001-02-05
FRIOR FILING DA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQS--QLKPRDLC 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 197; DB 8;
Pred. No. 3.7e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPV 31
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) OTHER INFORMATION: May be any amino acid

US-10-061-395-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90.8%;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 61.3%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41; Conservative
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Best Local Similarity
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28.1%; Score 61; DB 11; Length 1286; 38.2%; Pred. No. 4.7;

1 MLFNLRXXLNNAAFRHGHNFMVRNFRCGOPL 31

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APPLICANT: Terry, Roemer D.
APPLICANT: Terry, Roemer D.
APPLICANT: Tofarles, Boone
APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
TITLE REPERENCE: 10182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT PILLNG DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7102
LENGTH: 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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53;
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Pred. No. 77;
6; Mismatches 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
23.0%; Score 50; DB
Best Local Similarity 34.3%; Pred. No. 53;
Matches 12; Conservative 5; Mismatches
Sequence 7915, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OWURA, SATOSHI
APPLICANT: ISHIKAMA, UUN
APPLICANT: ISHIKAMA, UUN
APPLICANT: SHIKAMA, UUN
APPLICANT: SHIKAMA, UND
APPLICANT: SHIRAM, HROSHI
APPLICANT: SHIRAM, HROSHI
APPLICANT: SHIRAM, HROSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRAM, TADAYOSHI
APPLICANT: SHIRAM, TADAYOSHI
APPLICANT: OSCANTION
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPREBACE: 249-262
CURRENT APPLICATION NUMBER: US 2001-204089
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: UP 2001-272697
PRIOR PILING DATE: 2001-06-30
PRIOR PILING DATE: 2001-06-30
PRIOR PILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
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Povey, Sue
van Slegtenhorst, Marjon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7102, Application US/10032585
Publication No. US20030180953A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09950046A Patent No. US20020151701A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 29.1%;
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 LSNLRILLNKAALR-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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                                                                                                                                                                                                                                                                                       APPLICANT: D'Andrea, Alan
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS OF CANCER SUSCEPTIBILI
TITLE OF INVENTION: DEFECTIVE DNA REPAIR MECHANISMS AND TREATMENT THEREOF
TITLE OF INVENTION: DEFECTIVE DNA REPAIR MECHANISMS AND TREATMENT THEREOF
CURRENT APPLICATION NUMBER: US/10/165,099
PRIOR PELICATION NUMBER: US 09/999,027
PRIOR APPLICATION NUMBER: US 00/245,756
PRIOR APPLICATION NUMBER: US 00/245,756
PRIOR FILING DATE: 2000-11-03
NUMBER OF SEQ ID NOS: 352
NUMBER OF SEQ ID NOS: 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/10353856
Fublication No. US20030215794A1
GENERAL INFORMATION:
APPLICANT: Kawacka, Yoshihiro
APPLICANT: Neumann, Gabriele
APPLICANT: Neumann, Gabriele
APPLICANT: Wisconsin Alumin Research Foundation
TITLE OF INVENTION: Filovirus Vectors and No. US20030215794Alinfectious Filovirus-Bas FILE REFRENCE: 800.032US1
CURRENT APPLICATION NUMBER: US/10/353,856
CURRENT FILING DATE: 2003-01-29
PRIOR APPLICATION NUMBER: US 60/353,972
FRIOR APPLICATION NUMBER: US 60/353,972
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          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28.1%; Score 61; DB 12; Length 1286; 38.2%; Pred. No. 4.7;
     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Indels
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     14;
                                                                             107 SNLRRMLSSSSTTKRDESLVRNLLLVSPIQLDIQ 140
                                                 3 SNLRILLINKAALRKAHTSMVRNFRYGKPVQSQVQ 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 SNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQ 36
     7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
                                                                                                                                                                                                                      Sequence 3, Application US/10165099
Publication No. US20030188326Al
GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Reston Ebola virus
US-10-353-856-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 38.2
les 13; Conservative
13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
US-10-156-761-7915
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APPLICANT: Oblean, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Travick, John D.
APPLICANT: Travick, John D.
APPLICANT: Travick, John D.
APPLICANT: Transmoto, Robert T.
APPLICANT: Vanamoto, Robert T.
APPLICANT: Vanamoto, Robert T.
APPLICANT: Vanamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: Oblean: 00/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/201,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
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OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.7
OTHER INFORMATION: SWISSPROT HIT: P16960, EVALUE 3.00e-27
FRICK APPLICATION UNDER: 2001-01-30
PRICK APPLICATION UNDER: 2001-01-30
PRICK APPLICATION UNDER: 2001-01-30
PRICK APPLICATION UNDER: PCT/US01/00664
PRICK PILING DATE: 2001-01-30
PRICK FILING DATE: 2001-01-30
PRICK FILING DATE: 2001-01-30
PRICK APPLICATION UNDER: PCT/US01/00665
PRICK APPLICATION UNDER: PCT/US01/00668
PRICK APPLICATION UNDER: PCT/US01/00668
PRICK APPLICATION UNDER: PCT/US01/00663
PRICK APPLICATION WUMBER: PCT/US01/00663
PRICK APPLICATION WUMBER: PCT/US01/00661
PRICK APPLICATION WUMBER: PCT/US01/00661
PRICK APPLICATION WUMBER: PCT/US01/00661
PRICK APPLICATION WUMBER: PCT/US01/00661
PRICK APPLICATION WUMBER: PCT/US01/00670
PRICK APPLICATION WUMBER: BCT/US01/00670
PRICK APPLICATION WUMBER: US 09/608,408
PRICK PILING DATE: 2001-01-30
PRICK APPLICATION WUMBER: US 09/774,203
PRICK PILING DATE: 2000-06-30
PRICK APPLICATION WUMBER: US 09/774,203
PRICK PILING DATE: 2000-06-30
PRICK PILING DATE: 2001-01-29
PRICK PILING DATE: 2001-01-30
PRICK PILIN
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Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 40.0
Matches 14; Conservative
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Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: Compositions and Methods Based Upon the Tuberous Sclerosis-1 (TSC-1) Gene and Gene Product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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22.8%; Score 49.5; DB 10; Length 1164;
Best Local Similarity 29.8%; Pred. No. 2.2e+02;
Matches 14; Conservative 9; Mismatches 19; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |::||| | | | : | | | 806 MIAELRIELKKANNKVCHTELLLSQVSQKLSNSESVQQQMEFLNRQL 852
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Vinson & Elkins
STREET: 1455 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Sanzo, Michael A.
REGISTRATION NUMBER: 36,912
REFERENCE/DOCKET NUMBER: BRI331/42002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-6585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REPERRICE: Acondours. CENERATOR ANALISTS
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR PELING DATE: 2001-05-23
PRIOR PELING DATE: 2000-02-04
PRIOR PILING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-36
PRIOR FILING DATE: 2000-01-04
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2000-01-04
PRIOR PELING DATE: 2000-01-04
PRIOR PELING DATE: 2000-01-04
PRIOR PELING DATE: 2000-01-04
PRIOR PELING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PELING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/USO1/00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDENBESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                    CITY: Washington
STATE: D.C.
COUNTRY: U.S.
ZIP: 20004-1008
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1164 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (202) 639-6604 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                              NUMBER OF SEQUENCES: 28
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US-09-864-761-46024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 22.4%; Score 48.5; DB 9; Length 285; Best Local Similarity 34.9%; Pred. No. 57; Matches 15; Conservative 6; Mismatches 17; Indels 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITER. 011.A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-11-27
PRIOR PELING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
SOFTWARE: PASTSEQ for Windows Version 4.0
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10798, Application US/09815242
Patent No. US20020661569A1
GAPBRAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-23
PRIOR PELICH DATE: 2000-05-26
PRIOR PELICH DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-27
PRIOR FILING DATE: 2000-12-27
PRIOR FILING DATE: 2000-12-27
PRIOR FILING DATE: 2000-12-27
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US-09-815-242-10798
                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Enterococcus faecalis US-09-815-242-4869
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Best Local Similarity
--hes 15, Conservat
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LENGTH: 334
                                                                                                                                                                                                                                                                           SEQ ID NO 4869
LENGTH: 285
TYPE: PRT
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (221)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (223)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPRENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT APPLICATION ADMER: 2001-01-17
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: Patentin Ver. 2.0
LENGTH: 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 NSLHVLRNGSDILRRNEHHCWVFENF--NKPIDPPVRLGPRDI 116
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                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR APPLICATION NUMBER: UP 00/280988
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER: OF SEQ ID NOS: 7059
SEQ ID NO 3622
LENGTH: 684
                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Corynebacterium glutamicum
US-09-738-626-3622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4156, Application US/09764891; Publication No. US20030077808A1; GENERAL INFORWATION:
                                                    Sequence 3622, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
                                                                                                                               APPLICANT: NAKAGANA, SATOSHI
APPLICANT: NIZOGUCHI, HIROSHI
APPLICANT: ANDO, SELKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: CANTAI, KELKO
APPLICANT: CANTAI, KELKO
APPLICANT: TATEISHI, NACKO
APPLICANT: TATEISHI, NACKO
APPLICANT: SENDA, MASATO
APPLICANT: SKEDA, MASATO
APPLICANT: OZAKI, AKIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: SITE
LOCATION: (228)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-764-891-4156
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RESULT 14
US-09-738-626-3622
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us-08-765-244-22.rapb

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    LOCATION: (231)
    OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
    NAMENFKEY: SITE
    LOCATION: (234)
    OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
    US-09-764-891-4156
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	0; Gaps	
11; Length 235;	Described Similarity 37.0%; Fred. No. 54; Matches 10; Conservative 7; Mismatches 10; Indels	
B :	54; thes	10
Score 48;	Fred. No. 7; Mismato	9 LNKAALRKAHTSWVRNFRYGKPVQSQV 35
22.1%;	37.08; vative	HTSMVRNFR
	Conser	VKAALRKA
ch	10;	9
Query Mat	Matches	Qy

0

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Search completed: December 3, 2003, 14:35:35 Job time : 30 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

December 3, 2003, 14:30:02 ; Search time 21 Seconds (without alignments) 196.917 Million cell updates/sec

Run on:

US-08-765-244-22

Perfect score: Title:

1 MLSNLRILLNKAALRKAHTS.......NFRYGKPVQSQVQLKPRDLC 43

BLOSUM62 Scoring table:

Sequence:

283308 segs, 96168682 residues Searched:

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		*			SOFTWANTES	
Result		Query				
No.	Score	Match	Match Length	DB	QI	Description
н	199	91.7	354	٦	OWRT	ornithine carbamoy
7	164	75.6	354	Н	OWING	ornithine carbamoy
ო	141	65.0	354	-1	OWHU	ornithine carbamoy
4	119	54.8	41	(1	I52779	ornithine transcar
'n	61	28.1	1286		B71413	hypothetical prote
ø	9	27.6	351		F90409	GTP binding conser
7	S	26.3	354		JE0309	ornithine carbamoy
æ	55.5	25.6	454		A86345	F16F4.13 protein -
o,	55	25.3	350		A48421	ornithine transcar
10	η. 4.	24.9	300		T32702	hypothetical prote
11	54	24.9	457		AD0950	oxygen-independent
12	54	24.9	1225		A56514	chromokinesin - ch
13	53.5	24.7	425		140646	sensor-like protei
14	53	24.4	435	7	831290	cyclin B5 - yeast
15	53	24.4	593		T47000	nitrate/nitrite se
16	ın	24.4	593		AB0239	nitrate/nitrite se
17	52.5	24.2	185		B81708	translation elonga
18	52	24.0	213		B83182	probable two-compo
19	52	24.0	335		T33457	hypothetical prote
	52	4.	598		RGECNX	nitrate/nitrite se
21	52	24.0	598		F85702	nitrate/nitrite se
	LO.		598		G90844	nitrate/nitrite se
	51.5	m	260		G70233	hypothetical prote
	51	•	206		T50211	WD-repeat protein
	51	m.	598		AF0648	nitrate/nitrite se
	51	m,	633	N	S76749	hypothetical prote
27	51	23.5	705	7	S54521	probable membrane
	51	۳.	1779	7	m	hypothetical prote
29	50.5	23.3	138	~	F81900	

30 50.5 23.3 383 2 B83922 31 50.5 23.3 429 2 E90267 32 50 23.0 178 2 F91180 35 50 23.0 23.0 22 F91180 35 50 23.0 338 2 H75127 36 50 23.0 386 2 H75127 37 50 23.0 662 2 AB1979 38 49.5 22.8 164 2 T03814 49 52.6 176 2 S5740 43 49 22.6 351 2 H33068 44 49 22.6 446 2 C81719	short-chain-specif	hypothetical prote	hypothetical prote	hypothetical prote	motB homolog lafu	CAAX prenyl protei	probable molybdopt	signal recognition	calcium-dependent	cytochrome c PA303	purine NTPase [imp	tumor suppressor p	18c protein (clone	hypothetical prote	GTP-binding protei	conserved hypothet
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	23.3	23,3	23.0	23.0	23.0	23.0	23.0	23.0	23.0	22.8	22.8	22.8	22.6	22,6	22.6	22.6
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	3.0	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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ornithine carbamcyltransferase (EC 2.1.3.3) precursor - rat
NyAlternate names: citrulline phosphorylase; ornithine transcarbamylase
C;Specias: Ratus norvegicus (Norway rat)
C;Date: 28-Feb-1986 #sequence revision 28-Feb-1986 #text change 11-Jun-1999
C;Accession: A00563; A28042; A23090; S02466; I52976; I67609; I53457
F;Takkyguchi, M.; Miura, S.; Mori, M.; Tatibana, M.; Nagata, S.; Kaziro, Y.
Proc. Natl. Acad. Sci. U.S.A. 81, 7412-7416, 1984
A;Title: Molecular cloning and nucleotide sequence of cDNA for rat ornithine carbamoy)
A;Reference number: A00563; MUID:85063800; PMID:6095294

A;Accession: A00563

A; Molecule type: mRNA A; Residues: 1-354 < TAKI> A; Cross-references: GB: K03040; NID: 9205873; PIDN: AAA41768.1; PID: 9205874 A; Cross-references: GB: K03040; Nibra, S.; Mori, M. R; Takiguchi, M.; Murakani, T.; Miura, S.; Mori, M. Proc. Natl. Acad. Sci. U.S.A. 84, 6136-6140, 1987 A; Title: Structure of the rat ornithine carbamoyltransferase gene, a large, X chromosc A; Reference number: A28042; MUID: 87317609; PMID: 3476935

A; Accession: A28042

A, Molecule type: DNA
A, Readdues: 1-344 crax2>
A; Readdues: 1-344 crax2>
A; Readdues: 1-344 crax2>
A; Cross-references: GB:ML6933; GB:U02957; NID:g205884; PIDN:AA41769.1; PID:g205886
A; Cross-references: GB:ML6933; GB:U02957; NID:g205884; PIDN:AA41769.1; PID:g205886
B; Kraus, U.P.; Hodges, P.E.; Williamson, C.L.; Horwich, A.L.; Kalousek, P.; Williams, Nucleic, A.Dis. Res. 13, 943-952, 1985
A; Trile: A cDNA clone for the precursor of rat mitochondrial ornithine transcarbamylae
A; Reference number: A23090; WUID:85215524; PMID:3839075

A; Accession: A23090

A; Molecule type: mRNA
A; Residues: 1-38,'P',40-240,'S',242-354 < KRA>
A; Residues: 1-38,'P',40-240,'S',242-354 < KRA>
A; Cross-references: GB: X01976
B; Aoki, Y.; Sunaga, H.; Suzuki, K.T.
Biochem. J. 250, 735-742, 1988
A; Title: A cadmium-binding protein in rat liver identified as ornithine carbamoyltrans
A; Reference number: 802466; MUID:88268748; PMID:3390141

A;Molecule type: protein A;Residues: 33-56;293-302;307-317;322-329 <AOK> R;MCIntyre, P.; Graf, L.; Mercer, J.F.B.; Wake, S.A.; Hudson, P.J.; Hoogenraad, N. DNA 4, 147-156; 1985

A;Title: The primary structure of the imported mitochondrial protein, ornithine transc A;Reference number: IS2976; MUID:85203360; PMID:3838931 A;Accession: IS2976

A;Status: translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-354 <RES>

A;Cross-references: GB:M11266; NID:g205871; PIDN:AAA41767.1; PID:g205872
R;McIntyre, P.; Graf, L.; Mercer, J.; Peterson, G.; Hudson, P.J.; Hoogenraad, N.
FBBS Lett. 177, 41-46, 1984
A;Title: A highly basic N-terminal extension of the mitochondrial matrix enzyme ornit?
A;Reference number: I53457; MUID:85051832; PMID:6548714

us-08-765-244-22.rpr

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Query Match

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A; Molecule type: DNA
A; Residues: 1.36 kBE2>
A; Cross-references: GB:M1235; NID:g189408; PIDN:AAA59976.1; PID:g189409
A; Cross-references: GB:M1235; NID:g189408; PIDN:AAA59976.1; PID:g189409
R;Gilbert-Dussardier, B.; Rabier, D.; Strautnieks, S.; Segues, B.; Bonnefont, J.P.; Mu
Hum. Mol. Genet. 3, 831-832, 1994
A;Title: A novel arginine (245) to glutamine change in exon 8 of the ornithine carbamo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 26-276, 'Q', 278-289 <RE3>
A; Cross-references: GB:S73640; NID:g688001; PIDN:AAB31859.1; PID:g688002
A;Note: this sequence represents a disease defect in ornithine carbamoyltransferase C; Comment: The active enzyme is a dimer of identical chains with one tightly bound zin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for the nuclear coded precurs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hata, A.; Tsuzuki, T.; Shimada, K.; Takiguchi, M.; Mori, M.; Matsuda, I.
Biochem. 100, 717-725, 1986
Title: Isolation and characterization of the human ornithine transcarbamylase gene:
Reference number: I38078; WUID:87057134; PMID:3782067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PID:g219959
Kraus, J.P.; Doolittle,
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R;Wheeler, V.C.; Prodromou, C.P.; Pearl, L.H.; Williamson, R.; Coutelle, C.
Gene 169, 251-255, 1996
A;Title: Synthesis of a modified gene encoding human ornithine transcarbamylase
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A, Residues: 'M', 33-100, F', 102-110, 'P', 112-192, 'CF', 195-269, 'R', 271-354 < WHE>
A, Note: this report represents a synthetic gene designed for expression in (r. R, Horwich, A.L.; Kalousek, F.; Resenberg, L.E.
Proc. Natl. Acad. Sci. U.S.A. 82, 4930-4933, 1985
A, Title: Arginine in the leader peptide is required for both import and prote
                                                                                                                                                                                                                                                                                                                                                                                   NyAlternate names: citrulline phosphorylase, ornithine transcarbamylase Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cibate: 28-Feb-1986 #sequence revision 31-Mar-1993 #text change 16-Jun-2000
Cibaccession: A41444, B41444, A00562; I38078; J04672; I59039; I54377
R;Hata, A.; Tsuzuki, T.; Shimada, K.; Takiguchi, M.; Mori, M.; Matsuda, I.
A;Tille: Structure of the human ornithine transcarbamylase gene.
A;Reference number: A41444; MUID:88227905; PMID:2836378
                              Gaps
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A;Cross-references: GB:D00230; NID:g219957; PIDN:BAA00161.1; PID:g219959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecule type: mRNA
;Residues: 1-100,'F',102-110,'P',112-192,'CF',195-269,'R',271-354 <HOR>
;Cross-references: GB:D00230
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                           Indels
                                                                                                                                                                                                                                                                                                                                                        ornithine carbamoyltransferase (EC 2.1.3.3) precursor - human
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A;Fitle: Structure and expression of a complementary DNA for A;Reference number: A00562; MUID:84196410; PMID:6372096
                                                                                                    42
                                                                                                                                   1 MLSNLRILLINNAALRKGHTSVVRHFWCGKPVQSQVQLKGRDL
                                                                                            1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQLKPRDL
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                   Mismatches
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A;Status: translated from GB/EMBL/DDBJ
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                       5;
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                   Conservative
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A; Residues: 1-354 < HA2>
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                   35;
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                                                                                                    A,Cross-references: EMBL:X01178, NID:g56802, PIDN:CAA25618.1; PID:g56803
A,Accession: 153457
A,Accession: 153457
A,Accession: 153457
A,Accession: 153457
A,Molecule type: mENA
A,Residues: 143, N',45-99, R',101-102 cRE3>
A,Cross-references: GB:K03041; NID:g205889; PIDN:AA41771.1; PID:g205890
C,Genetics: 26/2, 72/3; 100/1; 129/2; 180/3; 221/3; 239/3; 289/3; 335/3
C,Superfamily: ornithine carbamoyltransferase; aspartate/ornithine carbamoyltransferase
F,1-32/Domain: transit peptide (mitochondrion) mitochondrion; transferase; urea cycle
F,1-32/Domain: transit peptide (mitochondrion) modicited cMPP-
F;33-354/Product: ornithine carbamoyltransferase #status predicted cMAT>
F;40-342/Domain: aspartate/ornithine carbamoyltransferase homology cACT>
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6224037; PMID:3011788
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A; Introns: 26/2; 72/3; 100/1; 129/2; 180/3; 221/3; 239/3; 289/3
C; Superfamily: ornithine carbamoyltransferase; aspartate/ornithine carbamoyltransferase
C; Keywords: mitochondrion; transferase; urea cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:M12716; NID:g200160; PIDN:AAA39864.1; PID:g554248
A;Note: the end of this sequence is near the boundary of the cloned region and may C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Date: 31-Mar-1993 #sequence_revision 13-Mar-1997 #text_change 11-Jun-1999 C;Accession: A43609; S34047; ISS222 R;Veres, G.; Gibbs, R.A.; Scherer, S.E.; Caskey, C.T. Science 237, 415-417, 1987 A;Title: The molecular basis of the sparse fur mouse mutation. A;Reference number: A43609; WUID:87263407; PMID:3603027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:M17030; NID:g200162; PIDN:AAA39865.1; PID:g200163 R;Scherer, S.E.; Veres, G.; Caskey, C.T.
Nucleic Acids Res. 16, 1593-1601, 1988
A;Title: The genetic structure of mouse ornithine transcarbamylase.
A;Reference number: S03407; MUID:B8157171; PMID:2831503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40-342/Domain: aspartate/ornithine carbamoyltransferase homology <ACT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;1-32/Domain: transit peptide (mitochondrion) #status predicted <TNP> F;3-335/Product: ornithine carbamoyltransferase #status predicted <MMT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ornithine carbamoyltransferase (EC 2.1.3.3) precursor - mouse N;Alternate names: citrulline phosphorylase; ornithine transcarbamylase (5;Species: Mus musculus (house mouse) (5;Species: Mus musculus (house mouse) (5;Date: 31-Mar-1993 #sequence_revision 13-Mar-1997 #text change 11-7nn-1 (5;Accession: A43609: An34/n. Fernis
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R;Veres, G.; Craigen, W.J.; Caskey, C.T.
Bibl. Cham. 261, 7588-7591, 1986
A;Title: The 5' flanking region of the ornithine transcarbamyl
A;Reference number: 155252; MUID:86224037; PMID:3011788
A;Status: translation not shown; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQLKGRDL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQLKPRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.7%; Score 199; DB 1; 97.6%; Pred. No. 9.3e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75.6%; Score 164; DB 1; 83.3%; Pred. No. 6.6e-15;
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-102 <RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Residues: 1-194,'R',196-335 <SCH>
Cross-references: EMBL:X07092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 41; Conserv
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Best Local Similarity
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Gene: OIC

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GTP binding conserved hypothetical protein SSO2385 [imported] - Sulfolobus solfataricu C;Species: Sulfolobus solfataricus C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
                                                                                                                                                                                                                                                                                                                                                                    Rishe, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Che Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, submitted to GenBank, April 2001
A; Description: Sulfolobus solfataricus complete genome.
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C;Superfamily: ornithine carbamoyltransferase; aspartate/ornithine carbamoyltransfera:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AE006641; NID:g13815687; PIDN:AAK42533.1; GSPDB:GN00155
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C.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 27-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;40-342/Domain: aspartate/ornithine carbamoyltransferase homology <AOC>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C,Species: Gallus gallus (chicken)
C,Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 351;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21; Indels
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S;Shimogiri, T.; Kono, M.; Mannen, H.; Mizutani, M.; Tsuji, J. Biochem. 124, 962-971, 1998
A;Title: Chicken ornithine transcarbamylase gene, structure, A;Reference number: JE0309; MUID:99011321; PMID:9792920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ornithine carbamoyltransferase (EC 2.1.3.3) - chicken
                                                                                                                           36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                           3 SNLRILLNKAALRKAHTSMVRNFRYGKPVOSQVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 60; DB 2
Pred. No. 1.7;
                       38.2%; Pred. No. 5.2;
tive 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 57; DB 2
Pred. No. 4.5;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Mismatches
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34.6%;
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Best Local Similarity 34.6:
Matches 18; Conservative
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Best Local Similarity 40.55
Matches 17; Conservative
                    Similarity 38.2
13; Conservative
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A, Accession: F90409
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A;Residues: 1-351 <KUR>
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A; Status: preliminary
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                       Best Local
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                                               Matches
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e synthesis of UMP.
C;Comment: The active enzyme catalyzes the condensation of carbamoyl phosphate and ornit C;Comment: The active enzyme catalyzes the condensation of carbamoyl phosphate and ornit A;Genetics GDB:UPS-1.1
A;Map position: Yp1.1.*Yp1.1.*
C;Superfamily: ornithine carbamoyltransferase; aspartate/ornithine carbamoyltransferase C;Keywords: arginine biosynthesis; homotrimer; mitochondrion; transferase; urea cycle F;1-32/Domain: transit peptide (mitochondrion) #status predicted <TNP>
F;33-354/Product: ornithine carbamoyltransferase #status predicted <MAT>
F;40-342/Domain: aspartate/ornithine carbamoyltransferase homology <ACT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein dl3525w - Arabidopsis thaliana
CiSpecies: Arabidopsis thaliana (mouse-ear cress)
A;Variery: columbia
C;Species: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 20-Jun-2000
C;Accession: B71413
R;Bevan, M; Bancroft, I.; Bent, B.; Mambutt, R.; Meitzenegger, T.; Pohl, T.M.; Terryn, N.; Giel P:; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.; Giel avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B. A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Pulgdomenech erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis than A;Reference number: A71400; MUID:98121113; PMID:9461215
A;Accession: B71413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28.1%; Score 61; DB 2; Length 1286;
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                                                                                                                                                                                                                                                                                                                                                                    9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MLFNLRILLINNAAFRNGHNFMVRNFRCGQPLQNKVQLKGRDL 42
                                                                                                                                                                                                                                                                                                                                                                                                                    1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQLKPRDL 42
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A;Residues: 1-1286 <BEV>
A;Cross-references: GB:Z97337; NID:g2244829; PID:g2244854
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Pred. No. 1.1e-09;
4; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                          Pred. No. 1e-11;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ornithine transcarbamylase peptide - rat (fragment)
                                                                                                                                                                                                                                                                                                                     Score 141;
                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 69.0%;
Matches 29; Conservative
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Best Local Similarity
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21-Jan-2000

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Gaps

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Query Match

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Best Loca Matches

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Chromokinesin - chicken
Cispecies: Gallus gallus (chicken)
Cispecies: Gallus gallus (chicken)
Cispecies: Gallus gallus (chicken)
Cispecies: Callus gallus (chicken)
Ciscession: A56514; I50691
Riwang, S. Z.; Adler, R.
J. Cell Biol. 128, 761-768, 1995
A; Title: Chromokinesin: a DNA-binding, kinesin-like nuclear protein.
J. Cell Biol. 128, 761-768, 1995
A; Title: Chromokinesin: a DNA-binding, kinesin-like nuclear protein.
A; Accession: A56514; MUID:95181533; PMID:7876303
A; Accession: A56514
A; Status: preliminary
A; Accession: A56514
A; Status: preliminary
A; Cross-references: GB:U18309; NID:g603760; PIDN:AAC59666.1; PID:g603761
R; Wang, S. Z.; Adler, R.
R; Mang, S. Z.; Adler, R.
Proc. Natl. Acad. Sci. U.S.A. 91, 1351-1355, 1994
A; Title: A developmentally regulated basic-leuine zipper-like gene and its expression
A; Accession: Teoco.
A; Accession: Teoco.
A; Accession: A53451; MUID:94151328; PMID:8108415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Riparkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churche th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farra Nature 413, 848-852, 2001
A,Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.A;Reference number: ABOSO2; MUID:21534947; PMID:11677608
A,Accession: ADOSO3
A,Accession: ADOSO3
A,Acture: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - Salmonella enterica sub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Molecule type: DNA
A,Residues: 1-457 <PAR>
A,Cross-references: GB:AL513382; PIDN:CAD03096.1; PID:g16504733; GSPDB:GN00176
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oxygen-independent coproporphyrinogen III oxidase [imported] - Salmonella er C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AD0950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: EMBL: U04821; NID: 9440792; PIDN: AAA18960.1; PID: 9440793
                                                                                                                                                                                                                                                                                     Gabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                A,Gene: CESP:C14C6.13
A,Map position: 5
A;Introns: 91/1; 129/2; 145/3; 267/3
C,Superfamily: Caenorhabditis elegans hypothetical protein C14C6.13
                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
                                                                                                                                                                                                          Query Match 24.9%; Score 54; DB 2; Length 300; Best Local Similarity 31.4%; Pred. No. 9.9; Matches 11; Conservative 10; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Length 457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Superfamily: oxygen-independent coproporphyrinogen oxidase
                                                                                                                                                                                                                                                                                                                                                                          15;
                                                                                                                                                                                                                                                                                                                                         2 LSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQ 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 728-1086, RI' <WA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 LNKAALRKAHTSMVRNFRYGKPVQSQVQLKPRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.9%; Score 54; DB 26.5%; Pred. No. 16; iive 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene: STY3877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genetics:
                   C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
A48421
cornithine transcarbamylase - bullfrog
cyspecies: Rana catesbeiana (bullfrog)
Cyspecies: Rana catesbeiana (bullfrog)
Cybace: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999
CyAccession: A48421
R/Helbing, C.; Gergely, G.; Atkinson, B.G.
RyHelbing, C.; Gergely, G.; Atkinson, B.G.
A/Fitle: Sequential up-regulation of thyroid hormone beta receptor, ornithine transcarba
ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

Nature 408, 816-820, 2000

Nature 408, 816-820, 2000

A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Roney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: liver
A; Note: sequence extracted from NCBI backbone (NCBIN:126154, NCBIP:126155)
C; Superfamily: ornithine carbamoyltransferase; aspartate/ornithine carbamoyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Molecule type: DNA
A,Residues: 1-300 <DAV>
A,Cross-references: EMBL:AF039051; PIDN:AAB94269.1; GSPDB:GN00023; CESP:C14C6.13
A,Experimental source: strain Bristol N2; clone C14C6
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                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross_references: GB:AE005172; NID;g8920642; PIDN:AAF81364.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein C14C6.13 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 04-Mar-2000
C;Accesion: T32702
R;David, M.; Wohldmann, P.; Bauer, C.; Antoniou, B.
submitted to the EMBL Data Library, December 1997
A;Description: The sequence of C: elegans cosmid C14C6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-350 <HEL>
A;Cross-references: GB:M95193; NID:g213683; PIDN:AAA49528.1; PID:g213684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ÷
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 25.3%; Score 55; DB 2; Length 350; Best Local Similarity 38.1%; Pred. No. 8.5; Matches 16; Conservative 9; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d thyroid hormone induced metamorphosis.
A.Reference number: A48421; MUID:93177976; PMID:1291156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 55.5; DB 2;
Pred. No. 9.6;
5; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||| : | | :|| :|| 422 KAAYSRTSTDSPSRNYRESQPMGSPVQARPR 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 KAALRKAHT-SMVRNFRYGKPVQSQVQLKPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25.6%;
45.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Conservative
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A, Status: preliminary
A, Molecule type: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-454 <STO>
                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
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RESULT 10

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A;Molecule type: DNA
A;Residues: 1-435 <UOH>
A;Ctoss-references: BMBL:U40828; NID:g1066467; PIDN:AAB68061.1; PID:g1066475; MIPS:YPF
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: strain 6/69
C; Superfamily: nitrate/nitrite sensor protein narX
C; Keywords: autophosphorylation; phosphohistidine; phosphoprotein; phosphotransferase;
F; 401/Active site: His (phosphohistidine intermediate) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RiBuchrieser, C.; Rusniok, C.; Couve, E.; Frangeul, L.; Billault, A.; Kunst, F.; submitted to the EMBL Data Library, October 1998
A;Description: DNA sequence of the 102 kbases unstable region of Yersinia pestis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Yersinia pestis
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nitrate/nitrite sensor protein (EC 2.7.3.-) [similarity] - Yersinia pestis
                                                                                                                                                                                                                                                                                                           24.4%; Score 53; DB 2; Length 435; 46.4%; Pred. No. 20; tive 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match . 24.4%; Score 53; DB 2; Length 593; Best Local Similarity 34.1%; Pred. No. 29; Matches 14; Conservative 8; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    450 LLTTFRLKLNEATLEAALQALVNEFSERAGLSITFKYQLPP 490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-593 < BDD.
A;Cross_references: EMBL:AL031866; PIDN:CAA21343.1
                                                                                                                                                                                                                                                                                                                                                                                                                     3 SNLRILLNKAALRKAHTSMVRNFRYGKP 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       completed: December 3, 2003, 14:34:18
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNLKILQNKRALSKNDSSSKQQVQDSKP
                                                                                                                                       A)Gene: SGD:CLBS, CLBS
A)Cross-references: SGD:S0006324
A)Map position: 16R
C,Superfamily: cyclin
C;Keywords: cell cycle control
                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: Z24348
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 13; Conserv
                   A;Accession: S69013
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C;Keywords: autophosphorylation; phosphohistidine; phosphoprotein
F;196-421/Domain: sensor histidine kinase homology <SHK>
F;227/Binding site: phosphate (His) (covalent) (by autophosphorylation) #status predicte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-435 < EBPS-
A; Residues: 1-435 < EBPS-
A; Cross-references: EMBL: M91209; NID:g171238; PIDN:AAA34503.1; PID:g171239
B; Schwob, E.; Naemyth, K.
Genes Dev. 7, 1160-1175, 1993
A; Title: CLB5 and CLB6, a new pair of B cyclins involved in DNA replication in Saccharom A; Reference number: S36228; MUID:93307652; PMID:8319908
A; Reference number: acid sequence not shown
A; Molecule type: DNA
C;Superfamily: unassigned kinesin-related proteins; kinesin motor domain homology C;Keywords: ATP; DNA binding; mitosis; nucleotide binding; P-loop F;11-344/Domain: kinesin motor domain homology <KMOT> F;88-95/Region: nucleotide-binding motif A (P-loop)
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                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
931290
cyclin B5 - yeast (Saccharomyces cerevisiae)
NyAlternate names: protein P9642.8; protein YPR120c
C;Species: Sacharomyces cerevisiae
C;Date: 28-May-1993 #sequence revision 28-May-1993 #text_change 19-Apr-2002
C;Accession, C.B.; Cross, F.R.
Genes Dev. 6, 1695-1706, 1992
A;Title: CLBS: a novel B cyclin from budding yeast with a role in S phase.
A;Reference number: S31290; MUID:92387544; PMID:1387626
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A;Cross-references: EMBL:X70435; NID:g396496; PIDN:CAA49893.1; PID:g396497
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                                                                                                                                             DB 2; Length 1225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.7%; Score 53.5; DB 2; Length 4 36.4%; Pred. No. 17; ... 10; Indels ive 10; Indels
                                                                                                                                       Score 54; DB 2; Length 122
Pred. No. 46;
9; Mismatches 15; Indels
                                                                                                                                                                                                                                                                               2 LSNLRILLNKA-ALRKA-HTSMVRNFRYGKPVQSQVQLKPRDL 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 311 IKILGRASALKRAFTNLLNNAIRYAKNVNVRIQ 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 IRILINKAALRKAHTSMVRN-FRYGKPVQSQVQ 36
                                                                                                                                          24.9%;
39.5%;
                                                                                                                                  Query Match
Best Local Similarity 39.5'
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 36.49
Matches 12; Conservative
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GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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sw model using - protein search, Ö

3, 2003, 14:17:57; Search time 11 Seconds (without alignments)
183.832 Million cell updates/sec December Run on:

US-08-765-244-22

217 1 MLSNLRILLNKAALRKAHTS.....NFRYGKPVQSQVQLKPRDLC Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result		Query				
No.	Score	Match	Length	DB	σī	Description
	1	, Q	354	+4	OTC RAT	P00481 rattus norv
7	164	75.6	354	Н	OTC_MOUSE	P11725 mus musculu
e	141	'n	354	ęН	OTC HUMAN	P00480 homo sapien
4	59	27.2	597	гH	IF2P METAC	
ហ	26	25.8	591	Н	IF2P_METMA	Q8pu78 methanosarc
9	55	'n,	350	М	OTC RANCA	
7	54	24.9	236	Н	RR2 LOTJA	Q9bbs6 lotus japon
ω	54	4.	457	Н	HEMN SALTY	
σ	54	24.9	1225	ч	KF4A_CHICK	
10	53	24.4	328	Н	OTC PIG	
11	53	24.4	435	Н	CGS5 YEAST	
12	52.5	***	185	Н	EFP1 CHLMU	Q9pkr6 chlamydia m
13	52			Н	NARX_ECOLI	
14	51	\sim		Н	POFB_SCHPO	Q09855 schizosacch
15	51	m		Н	YM37_YEAST	
16	51	m		٦	C9DA_BACTP	
17	50.5	~		Н	TRB2_SULSO	
18	20	m		Н	LAFU_VIBPA	
6 1	50	m		Н	SR68 CANFA	
20	20	\sim		Н	PRCA ANASP	Q59149 anabaena sp
21	φ.	N		٦	RASO_SULSO	Q97wh0 sulfolobus
22	49.5	\sim		Н	TSC1_RAT	Q9z136 rattus norv
23	σ,	\sim		,-1	TSC1_HUMAN	Q92574 homo sapien
24	49	N		Н	HEMN ECOLI	
25	49	\sim		Н	MYS5 YEAST	Q04439 saccharomyc
56	49	$^{\circ}$		Н	YHOO YEAST	P38800 saccharomyc
. 27	•	\sim		н	RYR1 PIG	P16960 sus scrofa
28	48.5	22.4	5037	Н	RYR1_RABIT	P11716 oryctolagus
29	æ.	CO.		Н	RYR1 HUMAN	
30	48	α		Н	R37A_SCHPO	
31	48	\sim		М	SYR BUCBP	P59483 buchnera ap
32	48	$^{\circ}$	9	m	PRCA ANAVA	anabaena
33	48	22.1	1025	н	BGAL_KLULA	P00723 kluyveromyc

Q8k9g1 buchnera ap P20740 gallus gall	Q66802 ebola virus P05733 schizosacch	Q9v122 pyrococcus	059219 pyrococcus	Q9ugi8 homo sapien	P47226 mus musculu	P10581 zea mays (m	P24607 pseudomonas	Q65952 canine aden	Q96685 canine aden
Y376_BUCAP OVOS_CHICK	RRPL_EBOSM R37B_SCHPO	PSMA_PYRAB	PSMA_PYRHO	TES HUMAN	TES MOUSE	RPOP MAIZE	T801 PSESH	VCOM ADECC	VCOM_ADECR
		Н	Н	-	H	н	ч	Н	П
333 1473	2210	260	260	421	423	1098	410	421	421
21.9	21.9	21.7	21.7	21.7	21.7	21.7	21.4	21.4	21.4
47.5	47.5	47	47	47	47	47	46.5	46.5	46.5
3.4 3.5	36 37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Biochem. J. 250:735-742(1988).
-!- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-ornithine = phosphate
                                                                                                                                                                                                                         [1] — SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=85063800; PubMed=6095294;
Takiguchi M., Miura S., Mori M., Tatibana M., Nagata S., Kaziro Y.;
"Molecular cloning and nucleotide sequence of cDNA for rat ornithine
                                                                                                                                                 Rattus norvegicus (Rat).
Bukaryota, Metacoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria; Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=85215524; PubMed=1839075;
Kraus J.P., Hodges P.E., Williamson C.L., Horwich A.L., Kalousek F., Williams K.R., Rosenberg L.E.;
Williams K.R., Rosenberg L.E.;
A. Chone for the precursor of rat mitochondrial ornithine transcarbamylase: comparison of rat and human leader sequences and
                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
OCT-2001 (Rel. 40, Last annotation update)
(OCTILITY CATABOOYLERASCERASE, mitochondrial precursor (EC 2.1.3.3)
(OCTILITY CONTINUE TRANSCARDAMYLASE).
                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Wistar; TISSUE=Liver;
MEDLINE=87317609; PubMed=3476935;
Takiguchi M., Murakami T., Miura S., Mori M.;
"Structure of the rat ornithine carbamoyltransferase gene, a large, chromosome-linked gene with an atypical promoter.";
Proc. Natl. Acad. Sci. U.S.A. 84:6136-6140(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aoki Y., Sunaga H., Suzuki K.T.; "A cadmium-binding protein in rat liver identified as ornithine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The primary structure of the imported mitochondrial protein, ornithine transcarbamylase from rat liver: mRNA levels during ontogenv.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-89203360; PubMed-3838931;
McIntyre P., Graf L., Mercer J.F.B., Wake S.A., Hudson P.J.,
Hoogenraad N.;
                                                                                                                                                                                                                                                                                                                       carbamoyltransferase precursor.";
Proc. Natl. Acad. Sci. U.S.A. 81:7412-7416(1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [5]
SEQUENCE OF 33-56; 293-302; 307-317 AND 321-329.
 354 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            conservation of catalytic sites.";
Nucleic Acids Res. 13:943-952(1985)
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=88268748; PubMed=3390141;
STANDARD;
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SEQUENCE FROM N.A.
                 P00481; Q63407;
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                                                                                                                                                                                                                                                                                      -!- PATHRAY: SECOND STEP IN UREA CYCLE, ARGININE BIOSYNTHESIS.
-!- SUBUNIT: Homotrimer.
-!- SUBCELLULAR LOCATION.
-!- SUBCELLULAR LOCATION.
-!- DISEASE: SPARSE FUR (SPF) MOUSE HAVE AN OTC WITH AN OVERALL.
-!- DECREASE IN ACTIVITY, AND ALTERED SUBSTRATE AFFINITY.
-!- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGREAMS; TIGRO06E8; orni carb tr; 1.
PROSITE; PS00097; CARBAMOYLTRANSPERASE; 1.
Arginine biosynthesis; Urea cycle; Transferase; Mitochondrion;
                                                                                [2]
SEQUENCE FROM N.A.
MEDLINE-88157717; PubMed=2831503;
SCHEFE S.E., Veres G., Caskey C.T.;
Scherer S.E., Veres G., Caskey C.T.;
"The genetic structure of mouse ornithine transcarbamylase.";
Nucleic Acids Res. 16:1593-1601(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32 MITOCHONDRION.
354 ORNITHINE CARBAMOYLTRANSFERASE.
263 BY SIMILARITY.
3703 BY SIMILARITY.
117 H -> N (IN SPARSE FUR MOUSE).
39765 MW; 33BBE5DIE88AA196 CRC64;
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75.6%; Score 164; DB 1; Length 354;
Best Local Similarity 83.3%; Pred. No. 8.8e-16;
Matches 35; Conservative 2; Mismatches 5; Indels
             Veres G., Gibbs R.A., Scherer S.E., Caskey C.T., "The molecular basis of the sparse fur mouse mutation."; Science 237:415-417(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGJ, MGI:97448; Otc.
InterPro; IPR006130; Asp/Orn COtranf.
InterPro; IPR006131; OTGace_0.
InterPro; IPR006131; OTGace_0.
InterPro; IPR006132; OTGace_P.
Pfam; PP00185; OTGace_P.
Pfam; PP0185; OTGace_N:
Pfam; PR0100; AOTGASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M17030; AAA39865.1; ---
EMBL; M12716; AAA39865.1; ---
EMBL; X07092; CAA30121.1; JOINED.
EMBL; X07094; CAA30121.1; JOINED.
EMBL; X07094; CAA30121.1; JOINED.
EMBL; X07095; CAA30121.1; JOINED.
EMBL; X07095; CAA30121.1; JOINED.
EMBL; X07099; CAA30121.1; JOINED.
EMBL; X07100; CAA30121.1; JOINED.
SMISS: 2DPAGE; P0174.
                                                                                                                                                                                                                                                   STRAIN=C57BL/6J;
MEDLINE=86224037; PubMed=3011788;
MEDLINE=87263407; PubMed=3603027;
                                                                                                                                                                                                                                                                                                                                                                                                     L-citrulline.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transit peptide.
TRANSIT 1
CHAIN 33
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ACT_SITE
VARIANT
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    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-0CT-1989 (Rel. 12, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Ornithine carbamoyltransferase, mitochondrial precursor (EC 2.1.3.3)
(OTCase) (Ornithine transcarbamylase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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PROSITE; PSO0097; CARBAMOYLTRANSFERASE; 1.

Arginine biosynthesis; Urea cycle; Transferase; Mitochondrion; Transit peptide.

1 32 MITOCHONDRION.

CHAIN 33 354 ORNITHINE CARBAMOYLTRANSFERASE.
                            PATHWAY: SECOND STEP IN UREA CYCLE, ARGININE BIOSYNTHESIS. SUBUNIT: Homotrimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORNITHINE CARBAMOYLTRANSFERASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
G -> P (IN REF. 3; AAA41772).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.7%; Score 199; DB 1; Length 354; 97.6%; Pred. No. 9.2e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQLKPRDL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MLSNLRILLINKAALRKAHTSMVRNFRYGKPVQSQVQLKGRDL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             156B511AF7063F0C CRC64;
                                                                     -i- SUBCELLULAR LOCATION: Mitochondrial matrix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nastronia properties and corrant. Interpro; IPR002292; Orn_carbtransf. Interpro; IPR006131; OTCace O. Interpro; IPR006131; OTCace O. Interpro; IPR006132; OTCace P. Pfam; PF00185; OTCace; I. Pfam; PF02729; OTCace N. 1.
                                                                                                                                                                                                                                                                                                                     EMBL, M16933, AAA41769.1;
EMBL, M16924, AAA41769.1;
EMBL, M16925, AAA41769.1;
UNIED. EMBL, M16926, AAA41769.1;
UNIED. EMBL, M16929, AAA41769.1;
UNIED. EMBL, M16929, AAA41769.1;
UNIED. M16939, AAA41769.1;
EMBL, M16930, AAA41769.1;
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EMBL; M16933; AAA41769.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0100; AOTCASE
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354
263
303
39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=C57BL/6J;
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                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, M16928; A EMBL, M16929; A EMBL, M16929; A EMBL, M16932; A EMBL, X01976; C EMBL, X00001; A
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ACT SITE
CONFLICT
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Matches

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Gaps

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42

1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQLKPRDL

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2.1.3.3

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Shi D., Morizono H., Aoyasi M., Tuchman M., Allewell N.M.; "Crystal structure of human ornithine transcarbamylase complexed with carbamoyl phosphate and L-norvaline at 1.9 A resolution.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Horwich A.L., Fenton W.A., Williams K.R., Kalousek F., Kraus J.P., Doollittle R.F., Konigsberg W., Rosenberg L.B., Structure and expression of a complementary DNA for the nuclear coded precursor of human mitochondrial ornithine transcarbamylase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIINE=87057134; PubMed=3782067;
Hata A., Tsuzuki T., Shimada K., Takiguchi M., Mori M., Matsuda I.;
"Isolation and characterization of the human ornithine
transcarbamylase gene: structure of the 5'-end region.";
J. Biochem. 100:717-725(1986).
                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=88227905, PubMed=2836378;
Hata A., Fatuzuki T., Shimada K., Takiguchi M., Mori M., Matsuda I.;
"Structure of the human ornithine transcarbamylase gene.";
J. Biochem. 103:302-308(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99069419; PubMed=9852088;
Shi D., Morizono H., Ha Y., Aoyagi M., Tuchman M., Allewell N.M.;
"1.85-A resolution crystal structure of human ornithine
                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transcarbamoylase complexed with N-phosphonacetyl-L-ornithine.
Catalytic mechanism and correlation with inherited deficiency.";
J. Biol. Chem. 273:34247-34254 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=85270440; PubMed=3895227;
Horwich A.L., Kalousek F., Rosenberg L.E.;
Harwinne in the leader peptide is required for both import and proteolytic cleavage of a mitochondrial precursor.";
Proc. Natl. Acad. Sci. U.S.A. 82:4930-4933(1985).
                                                                                                                                                                                          precursor (EC
                42
1 MLSNLRILLINNAALRKGHTSVVRHFWCGKPVQSQVQLKGRDL
                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
07-Care (Ornithine carbamoyltransferase, mitochondrial)
                                                                                                       Ā
                                                                                                       354
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MEDLINE=20274073; PubMed=10813810;
                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REVIEW ON VARIANTS.
MEDLINE=93372868; PubMed=8364586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=84196410; PubMed=6372096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jum. Mutat. 2:174-178(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 224:1068-1074(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         carbamoyl phosphate and L-1
Proteins 39:271-277(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-36 FROM N.A.
                                                                                                       STANDARD;
                                                                                                                                                                                                                                                Homo sapiens (Human).
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REVIEW ON VARIANTS
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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SEQUENCE OF 269-289 FROM N.A., AND VARIANT OTCD GLN-277.
MEDLINE=94362689; PubMed=8081373;
Gilbert-tussardier B., Rabier D., Strautnieks S., Segues B.,
Galbert-tussardier B., Rabier D., Strautnieks S., Segues B.,
"A novel arginine (245) to glutamine change in exon 8 of the ornithine carbamoyl transferase gene in two unrelated children presenting with late onset deficiency and showing the same enzymatic pattern.";
Hum. Mol. Genet. 3:831-832(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANTS OTCD GLN-26; PRO-45 AND GLU-216, AND VARIANT ARG-46. MEDLINE=89345570; PubMed=2474822; Grompe M., Muzny D.M., Caskey C.T.; Grompe M., Muzny D.M., Caskey C.T.; "Scanning detection of mutations in human ornithine transcarbamoylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Fatal hyperammonemia resulting from a C-to-T mutation at a MspI site of the ornithine transcarbamylase gene. ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93126062; PubMed=1480464;
Tuchman M., Holzknecht R.A., Gueron A.B., Berry S.A., Isai M.Y.;
"Six new mutations in the ornithine transcarbamylase gene detected by
single-strand conformational polymorphism.";
                                      human ornithine transcarbamylase
                                                                                                                                                                                                                                                                                                        Maddalena A., Spence J.E., O'Brien W.E., Nussbaum R.L.; "Characterization of point mutations in the same arginine codon in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=90269805; PubMed=2347583; Finkelstein J.B., Francomano C.A., Brusilow S.W., Traystman M.D., Finkelstein J.B., Francomano C.A., Brusilow S.W., Traystman M.D., Wilso of denaturing gradient gel electrophoresis for detection of mutation and prospective diagnosis in late onset ornithine transcarbamylase deficiency.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT OTCD PRO-140.
MEDLINE=93273296; PubMed=8099056;
MEDLINE=93273296; PubMed=8099056;
Tsai M.Y., Holzknecht R.A., Tuchman M.;
"Single-strand conformational polymorphism and direct sequencing applied to carrier testing in families with ornithine transcarbamylase deficiency.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=91118929; PubMed=1671317;
Grompe M., Caskey C.T., Fenwick R.G. Jr.;
"Improved molecular diagnostics for ornithine transcarbamylase
                                                                                                                  REVIEW ON VARIANTS, AND 3D-STRUCTURE MODELING.
MEDLINE=96091868; PubMed=8544185;
Tuchman M., Morizono H., Reish O., Yuan X., Allewell N.M.;
"The molecular basis of ornithine transcarbamylase deficiency:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANT OTCD LEU-225.
MEDLINE=92098086; PubMed=1721894;
Hentzen D., Pelet A., Feldman D., Rabier D., Berthelot J.,
                                                                                                                                                                                                modelling the human enzyme and the effects of mutations."; J. Med. Genet, 32:680-688(1995).
                                                                                                                                                                                                                                                                                                                                                 three unrelated patients with ornithine transcarbamylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANTS OTCD GLN-92 AND LEU-320, AND VARIANT PRO-111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANTS OTCD GLU-79; THR-94; PHE-304 AND ASP-345.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        by chemical mismatch cleavage.";
Proc. Natl. Acad. Sci. U.S.A. 86:5888-5892(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       deficiency.";
Am. J. Hum. Genet. 48:212-222(1991).
                   Tuchman M., Plante R.J.;
"Mutations and polymorphisms in the gene: mutation update addendum.";
                                                                                                                                                                                                                                                                                                                                                                                             Clin. Invest. 82:1353-1358(1988)
MEDLINE=95353279; PubMed=7627182;
                                                                                                                                                                                                                                                                                         MEDLINE=89008892; PubMed=3170748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pediatr. Res. 32:600-604(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genet. 88:153-156(1991).
                                                                                  Hum. Mutat. 5:293-295 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomics 7:167-172(1990).
                                                                                                                                                                                                                                                                        VARIANT OTCD GLN-141.
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597 AA.

STANDARD;

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Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
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                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
FEB-2003 (Rel. 41, Last amodation update)
Probable translation initiation factor IF-2.
                                                                                                                                                      Methanosarcina acetivorans.
                                                                                                                                                                                                                          NCBI TaxID=2214;
                                                                                                                                  INFB OR MA1525.
IF2P METAC
SOURCE SO
                                                                                 Tuchman M., Plante R.J., Giguere Y., Lemieux B.;
"The ornithine transcarbamylase gene: new 'private' mutations in four patients and study of a polymorphism.";
Hum. Mutat. 3:318-320(1994).
                                                                                                                                                                                                                                                                                                         "Four newly identified ornithine transcarbamylase (OTC) mutations (D126G, R129H, I172M and W332X) in Japanese male patients with earlyonset OTC deficiency.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIJINE=55038770; PubMed=7951259;
Tuchman M., Plante R.J., McCann M.T., Qureshi A.A.;
"Seven new mutations in the human ornithine transcarbamylase gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANTS OTCD MET-125, ARG-188; VAL-209 AND LEU-302.
MEDLINE=96400964; PubMed=8807340;
Gilbert-Dussardier B., Segues B., Rozet J.-M., Rabier D., Calvas P.,
Gilbert-Dussardier J.-P., Munnich A.;
"Partial duplication [dup. TCAC (178)] and novel point mutations
(T125M, G188R, A2209V, and H302L) of the ornithine transcarbamylase
gene in congenital hyperammonemia.";
Hum. Mutat. 8:74-76 (1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "A splicing mutation, a nonsense mutation (Y167X) and two missense mutations (1159T and A209V) in Spanish patients with ornithine transcarbamylase deficiency.";
                                                                                                                                                                                                VARIANTS OTCD GLY-126; HIS-129 AND MET-172.
MEDLINE=94362715; PubMed=8081398;
Matsurar T., Hoshide R., Kiwaki K., Komaki S., Koike B., Endo F.,
Oyanagi K., Suzuki Y., Kato I., Ishikawa K., Yoda H., Kamitani S.,
Sakaki Y., Matsuda I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANTS OTCD HIS-40; ASN-88; TYR-202 AND ASN-263.
Guardamagna O., Gatti E., Parini R., Plante R.J., Tuchman M.;
"Genotype-phenotype correlations in ornithine transcarbamylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Garcia-Perez M.A., Sanjurjo P., Briones P., Garcia-Munoz M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                             JARIANTS OTCD HIS-40; HIS-129; ARG-195; THR-225; GLN-277 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zimmer K.P., Matsuura T., Colombo J.-P., Koch H.G., Ullrich Deufel T., Harms E., Matsuda I.; "A novel point mutation at codon 269 of the ornithine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANTS OTCD ASN-88; CYS-176; ALA-220; TYR-302 AND LYS-343
MEDLINE-97114289; PubMed-8956038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 141; DB 1; Length 354; Pred. No. 1.7e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transcarbamylase (OTC) gene causing neonatal onset of OTC
                                              VARIANTS OTCD LEU-117; LEU-182 AND CYS-203.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         deficiency.";
J. Inherit. Metab. Dis. 18:356-357(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANTS OTCD THR-159 AND VAL-209.
MEDLINE=96070988; PubMed=8530002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96086561; PubMed=7474905;
                                                                     MEDLINE=94290509; PubMed=8019569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enzyme Protein 49:191-191(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hum. Genet. 96:549-551 (1995).
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Genet, 91:321-325(1993).
                                                                                                                                                                                                                                                                                                                                                                                   Hum. Mutat. 3:402-406(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANT OTCD GLU-269.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              deficiency."
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           255 ATLDVILYDGTLKKGDTVVIGSL--GEPIQTKVRALLKPREL 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 SNLRILLINKAALRKAHTSMVRNFRYGKPVQSQVQ--LKPRDL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67CAF4D902C1B8D5 CRC64;
                                                                                                                                                                                                                                                                                                                      Pfam; PF00009; GTP EFTU; 1.
Pfam; PF03144; GTP EFTU D2; 1.
TIGRRAMS; TIGR00491; aIF-2; 1.
TIGRPAMS; TIGR00231; small GTP; 1.
PROSTIR; PS01176; IR2; FALSE NEG.
Initiation factor; Protein biosynthesis; GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27.2%; Score 59; DB 333.3%; Pred. No. 1.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTP
                                                                                                                                                                                             HAMAÞ; MF_00100; -; 1.
InterPro; IPR000795; BF_GTPbind.
InterPro; IPR004161; BFTU_D2.
                                                                                                                                                                                                                                                             InterPro; IPR000178; IF2.
InterPro; IPR005225; Small GTP.
InterPro; IPR004544; IIF_aIF-2.
                                                                                                                                                                           EMBL; AE010822; AAM04939.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65438 MW;
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88
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ID IF2P METWA
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NP_BIND
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Gaps

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9; Indels 47

4; Mismatches

29; Conservative

Matches

1 MLFNLRILLINNAAFRNGHNFWYRNFRCGQPLQNKVQLKGRDL 42 1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQLKPRDL

RESULT 4 IF2P_METAC

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catesbeiana (Bull frog).
                                                                                                                                                                                                                                                                                                                                                                                          metamorphosis.";
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TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P00480;
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ACT_SITE
ACT_SITE
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RR2_LOTUA
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    엄
                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as along as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTC_RANCA STANDARD; PRT; 350 AA.
P31326;
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ornithine carbamoyltransferase, mitochondrial precursor (EC 2.1.3.3)
(OTCase) (Ornithine transcarbamylase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.
                                                                                                                                             Archaea, Euryarchaeota, Euryarchaeota orders incertae sedis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25.8%; Score 56; DB 1; Length 591; 33.3%; Pred. No. 3.7; Live 13; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TP (BY SIMILARITY).

TP (BY SIMILARITY).

TP (BY SIMILARITY).

FE328265BBD887DF CRC64;
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                                                                                                                                                              Methanosarcinales; Methanosarcinaceae; Methanosarcina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGREAMS; TIGRO0491; aIF-2; 1.
TIGREPMS; TIGRO0231; small GTP; 1.
PROSTIE; PS01176; IF2; FALSE NEG:
Initiation factor; Protein blosynthesis; GTP-binding;
                     28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable translation initiation factor IF-2.
                                                                                                   INFB OR MM2463.
Methanosarcina mazei (Methanosarcina frisia)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAMAR, MF 00100; -; 1.
INTERPO, IPRO00795; BF GTPbind.
INTERPO, IPRO04161; BFTU_D2.
INTERPO; IPRO0525; Small GTP.
INTERPO; IPRO6525; Small GTP.
INTERPO; IPRO6544; ITF aTF-2.
Pfam; PF00009; GTP_EFTU; 1.
Pfam; PF00144; GTP_EFTU; 1.
Pfam; PF00144; GTP_EFTU; 1.
PRINTS; PR00315; ELONGATNFCT.
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919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 33.3. es 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome.
                                                                                                                                                                               NCBI_TaxID=2209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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SOURCE STATE SOURCE SOURCE SOURCE STATE SOURCE SOUR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rep. Fac. Sci. Shizouka Univ. 29:45-54 (1995).
-!- FUNCTION: OTC IS NECESSARY FOR THE TADPOLES TEANSITION FROM AN AMMONOTELIC, AQUATIC LARVA TO A UREOTELIC, TERRESTRIAL ADULT.
-!- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-ornithine = phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBI_TaxID=8400;
                                                                                                                                                                                                                                       Helbing C., Gergely G., Akkinson B.G., Sequential up-regulation of thyroid hormone beta receptor, ornith transcarbamylase, and carbamyl phosphate synthetase mRNAs in the liver of Rana catesbeiana tadpoles during spontaneous and thyroid hormone-induced metamorphosis.";

Dey. Genet. 13:289-301(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- PATHWAY: SECOND STEP IN UREA CYCLE, ARGININE BIOSYNTHESIS.
-!- SUBUNIT: Homotrimer.
-!- SUBCELLULER LOCATION: Mitochondrial matrix.
-!- TISSUE SPECIFICITY: LIVER.
-!- DEVELOPMENTAL STAGE: EXPRESSED DURING EMBRYONIC DEVELOPMENT.
-!- INDUCTION: By thyroid hormone.
-!- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4
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PROSITE; PS00097; CARBAMOYLTRANSFERASE; 1.
Arginine biosynthesis; Urea cycle; Transferase; Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Iwase K., Yamanchi K., Ishikawa K.;
"Molecular cloning of bullfrog (Rana caresbeiana) ornithine
transcarbamylase and induction of its mRNA during spontaneous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MITOCHONDRION (BY SIMILARITY).
ORNITHING CARBAMOYLTRANSFERASE.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.3%; Score 55; DB 1; Length 350; 38.1%; Pred. No. 2.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E1E598355F03C13E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQLKPRDL 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR006130; Asp/orn Cotranf.
InterPro; IPR002292; Orn carbtransf.
InterPro; IPR006131; OTCace O.
InterPro; IPR006132; OTCace P.
                                                                                                                                                                                                                  MEDLINE=93177976; PubMed=1291156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39636 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M95193; AAA49528.1; -.
EMBL; D38304; BAA22775.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00185; OTCace; 1.
Pfam; PF02729; OTCace N; 1.
PRINTS; PR00100; AOTCASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  350
259
299
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                                                                                                                                                                                                                                                                    Eukarycta, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids 1; Fabales; Fabaceae; Papilionoideae; Loteae; Lotus.
NCBI_TaxID=34305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAINN-Accession MG-20;
MEDLINB-21082929; PubMed=11214967;
Karo T., Kaneko T., Sato S., Nakamura Y., Tabata S.;
"Complete structure of the chloroplast genome of a legume, Lotus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  japonicus.";
DNA Res. 7:323-330(2000).
-!- SIMILARITY: BELONGS TO THE S2P FAMILY OF RIBOSOWAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2;
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01-OCT-1994 (Rel. 30, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Oxygen-independent coproporphyrinogen III oxidase (EC 1....-)
(Coproporphyrinogense) (Coprogen oxidase).
HERN OR STM4004 OR STY3877 OR T3617.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xu K., Elliott T.;
"Cloning, DNA seguence, and complementation analysis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.9%; Score 54; DB 1; Length 236; 38.5%; Pred. No. 2.6; ive 10; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAMAR, MF 00291, -; 1.
INTERPRO, IPR001865; Ribosomal_S2.
INTERPRO, IPR001865; Ribosomal_S2.
INTERPRO, IPR001865; RIBOSOMĀLS2.
PFam, PF00318; Ribosomāl_S2, 1.
PRINTS; PR00395; RIBOSOMĀLS2.
TIGRFRAM; TIGRO1011; RPSB bact; 1.
PROSITE; PS00962; RIBOSOMĀL_S2_1; 1.
PROSITE; PS00962; RIBOSOMĀL_S2_2; 1.
Ribosomal protein; Chloroplāst_2, 1.
SEOUENCE 236 AA; 26982 WW; CE9E238572325586 CRC64;
                                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Chloroplast 30s ribosomal protein S2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      457 AA.
   236 AA
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MEDLINE=94252986; PubMed=8195073;
   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AP002983; BAB33197.1; -.
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Best Local Similarity 38.3...
Local Similarity 38.3...
Local Similarity 38.3...
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   STANDARD;
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                                                                                                                                                                                                                             japonicus.
                                                                                                                                                                                                                                                          Chloroplast
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   LOTJA
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HEMN_SALTY
                                                                                                                                                                                                                             Lotus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931; MEDLINE=22531367; PubMed=12644504; Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J., Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R., "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Bacteriol. 185:2330-2337 (2003).
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-:- COFACTOR: REQUIRES MAGNESIUM, ATP AND NAD (OR NADP) FOR ACTIVITY.
-:- PATHWAY: POTDMYIN blosynthesis.
-:- SUBCELLULAR LOCATION: Cytoplasmic.
-:- SIMILARITY: BELONGS TO THE ANAEROBIC COPROPORPHYRINOGEN III
OXIDASE FAMILY.
                                                                                                                                                                                                                                                         McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D. Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.; "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES S. typhi; STRAIN=CT18; MBDLINE=215347; PubMed=11677608; MBDLINE=2153447; PubMed=11677608; Parkhill 3.0 Dougan G., James K.D., Thomson N.R., Pickard D., Wain J. Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brocks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quall M., Rutherford K., Simmonds M., Skelton J., Stevens K., "Complete genome sequence Of a multiple drug resistant Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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0
                                                                                                                                                                             SPECIES=S.typhimurium, STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 26.5%; Pred. No. 5.3; 9; Conservative 10; Mismatches 15; Indels
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Porphyrin biosynthesis; Oxidoreductase; Magnesium; NAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          457 AA; 52828 MW; 5667B4FE76204DAB CRC64;
Salmonella typhimurium hemN gene encoding a putative oxygen-independent coproporphyrinogen III oxidase.", J. Bacteriol. 176:3196-3203(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, U06779; AAA19690.1; -.
EMBL, AAL022843.1; -.
EMBL, AL627280; CAD03096.1; -.
EMBL, AE01280; AAO71118.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enterica serovar Typhi CT18.";
Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF04055; Radical SAM; 1.
SMART; SM00729; Elp3; 1.
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InterPro; IPR006638; Elp3.
InterPro; IPR004558; HemN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 413:852-856(2001).
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Best Local Similarity
Matches 9; Conserv
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3

Gaps

7

15; Indels

Mismatches

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17; Conservative
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ACT_SITE
SEQUENCE
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019072;
      Matches
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Proc. Natl. Acad. Sci. U.S.A. 91:1351-1355(1994).
-!- FUNCTION: REQUIRED FOR MITOTIC CHROMOSOWAL POSITIONING AND BIPOLAR SPINDLE STABILIZATION.
-!- SUBCELLULAR LOCATION: NUCLEAR, ASSOCIATED WITH MITOTIC
                                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Chromokinesin: a DNA-binding, kinesin-like nuclear protein.";
J. Cell Biol. 128:761-768(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, AND TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NEUROEPITHELIUM OF EMBRYOS.
-!- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY.
CHROMOKINESIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 1225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- TISSUE SPECIFICITY: EXPRESSED IN PROLIFERATING CELLS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KG -> RI (IN REF. 2).
MW; FA01ED83425F5875 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KINESIN-MOTOR.
COILED COIL (BY SIMILARITY)
GLOBULAR.
ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00129; KISC; 1.
PROSITE; PS00411; KINSEIN MOTOR DOMAIN1; 1.
PROSITE; PS50067; KINSEIN MOTOR DOMAIN2; 1.
MOTOR PROTEIN; Microtubules; ATF-binding; DNA-binding;
                                                                                                                                                                               090640; 090608;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Chromosome-associated kinesin KIF4A (Chromokinesin).
                           LNKAALRKAHTSMVRNFRYGKPVQSQVQLKPRDL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 728-1088 FROM N.A.
STRAIN-White leghorn; IISSUE=Embryonic retina;
MEDLINE=94151328; PubMed=8108415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-White leghorn; TISSUE=Embryonic retina; MEDLINE=95181533; Pubmed=7876303;
                                                                                                                                                              PRT; 1225 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 54; DB
Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP, P17119; 3KAR.
INTERPRO, IPR001723, kinesin_motor.
PFam, PF00225, kinesin_1.
PRINTS; PR00380; KINESINHEAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nuclear protein; Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U18309; AAC59666.1; -.
EMBL; U04821; AAA18960.1; -.
PIR; A56514; A56514.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.9%;
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                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang S.Z., Adler R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1087 108
1225 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang S.Z., Adler R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHROMOSOMES
                                                                                                                                                              CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NP BIND
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Koger J.B., Jones B.E.;
"Nucleotide sequence of porcine OTCase cDNA.";
J. Anim. Sci. 75:3368-3368(1997).
-!- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-ornithine = phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                               15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Contithine carbamoyltransferase, mitochondrial precursor (EC 2.1.3.3)
(OTGase) (Ornithine transcarbamylase) (Fragment).
                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Suina, Suidae, Sus.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                          528 MSKELVELNKALALKEALAKKMIQNDSQLEPIQSOYOTNIKDL 570
2 LSNLRILLNKA-ALRKA-HTSMVRNFRYGKPVQSQVQLKPRDL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89302B9A471CD265 CRC64;
                                                                                                                                                          328 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR00293; Asp/Orn_Cotranf.
InterPro; IPR002292; Orn_carbEransf.
InterPro; IPR006131; OrCace O.
InterPro; IPR006132; OrCace_P.
Pfam; PF00185; OrCace; 1.
Pfam; PF001295; OrCace N.
Pfam; PF001209; AOTCASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98080180; PubMed=9420013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36738 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Y13045; CAA73480.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GQPLQNKVQLKGRDL 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28 GKPVQSQVQLKPRDL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10; Conservative
                                                                                                                                                          STANDARD;
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237
277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                       Sus scrofa (Pig)
                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P00480;
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RESULT 11

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EMBL; U40828; AAB68061.1; -.
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EFP1 CHLMU
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MEDLINE=97313271; PubMed=9169875;

MEDLINE=97313271; PubMed=9169875;

MEDLINE=97313271; PubMed=9169875;

MATAUJO R., Aparicio A., Barrell B.G. Badcock K., Benes V.,

A Araujo R., Aparicio A., Barrell B.G. Badcock K., Benes V.,

Bussey H., Storcher C.M., Coster F., Davis K., Benes V.,

Chung E., Churcher C.M., Coster F., Davis K.,

Dietrich F.S., Delius H., DiPaolo T., Dubois E., Duesterhoeft A.,

Dietrich F.S., Delius H., DiPaolo T., Dubois E., Duesterhoeft A.,

Duncan M., Flochh M., Fortin N., Friesen J.D., Fritz C.,

Hall J., Hebling U., Heumann K., Hilbert H., Hillier L.,

Hunicke-Smith S., Hyman R., Johnston M., Xalman S., Kleine K.,

Marathe R., Messenguy F., Mewes H.-W., Mirripati S., Moestl D.,

Marathe R., Messenguy F., Mewes H.-W., Mirripati S., Moestl D.,

Mueller-Auer S., Namath A., Nentwich U., Oefner P., Pearson D.,

Mueller-Auer S., Namath A., Nentwich U., Schaffe M.,

Schroens B., Schramm S., Schroeder M., Sdicu A.M., Tettellin H.,

Urrestarazu L.A., Ushinsky S., Vierendeels F., Vissers S., Voss H.,

Walsh S.V., Wambutt R., Wang Y., Wedler E., Wedler H., Winnett E.,

Zhong W.W., Zollner A., Vo D.H., Hani J.;

Nath R. M., Mentwe 187103-105 (1997).

Nath R. M., Mentwe 187103-105 (1997).

Nath R. M., Mentwe 187103-105 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Epstein C.B., Cross F.R.;
"CLB5: a novel B cyclin from budding yeast with a role in S phase.";
Genes Dev. 6:1695-1706(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -(- FUNCTION: REQUIRED FOR BFFICIENT PROGRESSION THROUGH S PHASE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WITH CDC28.
DEVELOPMENTAL STAGE: MAXIMALLY EXPRESSED. JUST BEFORE CELL CYCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schwob E., Nasmyth K.; "CLBS and CLBS, a new pair of B cyclins involved in DNA replication in Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POSSIBLY FOR THE NORMAL PROGRESSION THROUGH MEIOSIS. INTERACTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=94074493; PubMed=8253070;
Kuehne C., Linder P.;
"A new pair of B-type cyclins from Saccharomyces cerevisiae that function early in the cell cycle.";
EMBO J. 12:3437-3447(1993).
                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomycetales;
                                                                                                         01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
2-phase entry cyclin 5.
CLBS OR YPR120C OR P9642.8.
                                           435 AA.
                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=BF264-15D;
MEDLINE=92387544; PubMed=1387626;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=93307652; PubMed=8319908;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genes Dev. 7:1160-1175(1993).
                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=AB320;
                                           YEAST
                                           CGS5 YE?
P30283;
CGS5_YEAST
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Nucleic Acids Res. 28:1397-1406(2000).
Nucleic Acids Res. 28:1397-1406(2000).
-!- FUNCTION: INVOIVED IN PEPTIDE BOND SYNTHESIS. STIMULATES EFFICIENT
-- TRANSLATION AND PEPTIDE-BOND SYNTHESIS ON NATIVE OR RECONSTITUTED
70S RIBOSOMES IN VITRO. PROBABLY PUNCTIONS INDIRECTLY BY ALTERING
THE APPLINTLY OF THE RIBOSOME FOR AMINOACYL-TRNA, THUS INCREASING
THEIR REACTIVITY AS ACCEPTORS FOR PEPTIDYL TRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=MOPN / Niggs;
MEDLINE=20150255; PubMed=10684935;
MEDLINE=20150255; PubMed=10684935;
Read T.D., Brundam R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Bisen J., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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0
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Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=83560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BY SIMILARITY).
-!- PATHWAY: Protein biosynthesis.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the elongation factor P family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.4%; Score 53; DB 1; Length 435; 46.4%; Pred. No. 7; ive 4; Mismatches 11; Indels
                            SGD; S0006324; CLBS.
GO; GO:0005634; C:nucleus; IDA.
GO; GO:000082; P:G1/S transition of mitotic cell cycle;
GO; GO:000086; P:G2/M transition of mitotic cell cycle;
GO; GO:00006279; P:premeiotic DNA synthesis; IGI.
                                                                                                                                                                                                                                                                                                  Pfam; PF00134; cyclin; 1.
Pfam; PF02984; cyclin; 2.
SMART; SM00392; CYCLIN; 2.
Cyclin; Cell cycle, Cell division; Multigene family.
SEQUENCE 435 AA; 50431 MW; 5AD67EB841BA5759 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Elongation factor P 1 (EF-P 1).
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                                                                                                                                                                                                 InterPro; IPR006670; Cyclin.
InterPro; IPR004367; Cyclin Cterm.
InterPro; IPR006671; Cyclin N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
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HAMAP; MF_00141; -; 1.
InterPro; IPR001059; EF-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 46.4
Matches 13, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
PIR; S31290; S31290.
SGD; S0006324; CLB5.
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SEQUENCE FROM N.A.
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SPECIES.E..col; STRAINEK12;
MEDLINE=97061202; PubMed=8905232;
MEDLINE=97061202; PubMed=8905232;
Noshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SPECIESE.coli, STRAIN=K12;
MEDLINE=89263708; PubMed=2657652;
Mohno T., Noji S., Taniquchi S., Saito T.;
"The narX and narL genes encoding the nitrate-sensing regulators of Escherichia coli are homologous to a family of prokaryotic two-component regulatory genes.";
Nucleic Acids Res. 17:2947-2957(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES=E.COli; STRAIN=X12 / MG1655; MEDLINE=97426617; PubMed=9278503; Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Maynew J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
SPECISS=E.COli; STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Per G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map."; DNA Res. 3:137-155(1996).
                                                                                                                                                                  3,
                                                                                                                    Length 185;
                        PROSITE; PS01275; EFP; 1.
Protein biosynthesis; Elongation factor; Complete proteome.
SEQUENCE 185 AA; 20468 MW; 969BD834F4997CE2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                  Indels
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01-AUG-1992 (Rel. 23, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Nitrate/nitrite sensor protein narX (EC 2.7.3.-).
NARX OR NARR OR B1222 OR Z1998 OR ECS1727 OR SF1225.
                                                                                                                    DB 1;
                                                                                                                                                                                                                42
                                                                                                                                                                                                                                        Query Match
24.2%; Score 52.5; DE
Best Local Similarity 41.2%; Pred. No. 3.2;
Matches 14; Conservative 9; Mismatches
                                                                                                                                                                                                                11 KAALRKAHTSMV--RNFRYGKPVQSQVQLKPRDL
                                                                                                                                                                                                                                                                                                                                                                             598 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enterobacteriaceae; Escherichia.
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Escherichia coli 0157:H7, and
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                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
  Pfam; PF01132; EFP; 1.
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P10956;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                SPECIESE.Coli; STRAIN=0157:H7 / RIMD 0509952;
MEDLIRE=21156231; PubMed=11258796;
MEDLIRE=21156231; PubMed=11258796;
MAXIND K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and 0157."; Nucleic Acids Res. 30:4432-4441 (2002).

-!- FUNCTION: ACTS AS A SENSOR FOR NITRATE/NITRITE AND TRANSDUCES SIGNAL OF NITRATE AVAILABILITY TO THE NARL PROTEIN AND OF BOTH NITRATE OF THE NARP PROTEIN. NARX PROBABLY ACTIVATES NARL PROYED BY PHOSPHORYLATION IN THE PRESENCE OF NITRATE. NARX ALSO PLAYS A NEGRITUE ROLE IN CONTROLLING NARL ACTIVITY, PROBABLY THROUGH DEPHOSPHORYLATION IN THE ABSENCE OF NITRATE.
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Jin Q., Yuan Z., Xu J., Mang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-55 FROM N.A.
SPECIES=E.coli, STRANN=K12;
MEDLINE=89338707; PubMed=2668029;
Moji S., Nohno T., Saito T., Taniguchi S.;
"The nark gene product participates in nitrate transport induced in Escherichia coli nitrate-respiring cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES-E.coli; STRAIN-K12;
MEDLINE-89197902; Pubmed-2649492;
Stewart V., Parales J. Jr., Merkel S.M.;
"Structure of genes narL and narK of the nar (nitrate reductase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-60 FROM N.A. SPECIES=E.coli; STRAIN=K12 / MC4100; Cavicchioli R., Gunsalus R.P., Chiang R.C.; Submitted (AUG-1992) to the EMBL/GenBank/DDBJ databases.
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-!- SIMILARITY: Contains 1 histidine kinase domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Bacteriol. 171:2229-2234(1989)
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[5]
SEQUENCE F
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XM37_XEAST
ID YM37_XEAST
AC Q038Z4;
DT 01-NOV-1997
DT 01-NOV-1997
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01-NOV-1997
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Matches
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GSAHAINKAGS -> AAPWRSTKRDA (IN REF. 1 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Katayama S., Kitamura K., Lehmann A., Nikaido O., Toda T., "Fission yeast F-box protein Pof3 is required for genome integrity and
                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
                                                                                                                                                                                                                                                                                                                                                                2;
                                                                                                                                       PROSITE; PS50885, HAMP; 1.
PROSITE; PS50109; HIS KIN; 1.
Sensory transduction; Transferase; Kinase; Phosphorylation; Transmembrane; Inner membrane; Nitrate assimilation;
                                                                                                                                                                                                                                                                                                                                         24.0%; Score 52; DB 1; Length 598; 31.0%; Pred. No. 14; ive 9; Mismatches 18; Indels
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886BA0FC2C8F3C3E CRC64;
                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL) HAMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                                                                                                                                                          POTENTIAL.
PERIPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                HISTIDINE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            POFB SCHPO STANDARD; PRT; 506 AA. 009855; 09PTV1; 16-PEB-1996 (Rel. 33, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                POTENTIAL.
                                      IncerPro; IPR003594; ATPbind ATPase.
IncerPro; IPR003669; HAMP.
InterPro; IPR003661; His kinh.
InterPro; IPR005467; His kinh.
InterPro; IPR005467; His kinhse.
Pfam; PF00672; HAMP; 1.
SWART; SW00304; HAMP; 7.
SWART; SW00384; HATPase c; 1.
SWART; SW00387; HATPase c; 1.
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POF11 OR SPAC29E6.01 OR SPAC30.05.
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MEDLINE=21668955; PubMed=11809834;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mol. Biol. Cell 13:211-224(2002).
                                                                                                                                                                                                                                                                                                                    67083 MW;
                                                                                                                                                                                                                                                                                                                                                 Local Similarity 31.0
les 13; Conservative
                               EcoGene; EG10646; narx.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces.
NCBI TaxID=4896;
          G90844; G90844
S26137; RGECNX
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598 AA;
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                                                                                                                                                                                     Complete proteome
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Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., A Cliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E., Rutherford K., Rutter S., Saunders D., Seeger K., Slarp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Woodward J., Volkeart G., Aert R., Robben J., Grymonprez B., Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Bger P., Zimmermann W., Wedler H., Reinhardt R., Purnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Albert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dowen T., Mocemo S., Armstrong J., Forsburg S.L., Cower T., McCombie W.R., Paulsen I., Potashkin J., The genome sequence of Schizosaccharomyces pombe.";

M. Nather 415,812-880 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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(Rel. 35, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: Contains 1 F-box domain.
-!- SIMILARITY: Contains 7 WD repeats.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00678; WD REPEATS 1; 3.
PROSITE; PS50082; WD_REPEATS 2; 6.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F-BOX
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MD 2.
MD 4.
MD 5.
MD 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB061694; BAB55543.1; -. BMBL; AL36538; CAB64646.1; -. EMBL; Z66525; CAA91423.1; -. PIR; T50211; T50211; T50211; T50212; SPAC2986.01; -. InterPro; IPR001810; P-box. InterPro; IPR001810; WHO40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00320; GPROTEINBRPT.
ProDom; PD0000018; WD40; 1.
SWART; SW00326; PBOX; 1.
SWART; SW00320; WD40; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58257 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00646; F-box; 1.
Pfam; PF00400; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                      Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T., Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S., Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.; Wiltenucleotide sequence of Saccharomyces cerevisiae chromosome XIII.",
15-SEP-2003 (Rel. 42, Last annotation update)
Hypothetical 81.5 kDa protein in HLJ1-SMP2 intergenic region.
YMR163C OR YM8520.12C.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungei; Ascomycota; Saccharomycetina; Saccharomycetales;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23.5%; Score 51; DB 1; Length 705; 36.8%; Pred. No. 23; tive 5; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; S54521; S54521.
SGD; S0004773; YMR163C.
Hypothetical protein.
SEQUENCE 705 AA; 81466 MW; E4F2A4D205A98F66 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z49705; CAA89799.1; -.
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Best Local Similarity 36.88
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                Nature 387:90-93(1997)
                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=S288c / AB972;
PubMed=9169872;
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Search completed: December 3, 2003, 14:32:56 Job time: 12 secs

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0; Gaps

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RESULT 1
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Q8r188 mus musculu
Q8r10. bos taurus
Q63786 rattus norv
Q9iau8 trachemys s
Q9iau8 trachemys s
Q9iau8 trachemys s
Q97w5 sulfolobus
Q97w5 sulfolobus
Q97w9 gallus gall
Q9z635 streptococc
Q91mm3 arabidopsis
Q84x79 caenorhabdi
Q8ax79 caenorhabdi
Q8ax79 caenorhabdi
Q8ax79 drosophila
Q99pg3 drosophila
                                                                                                                                                             December 3, 2003, 14:29:02; Search time 34 Seconds (without alignments) 326.361 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                    1 MLSNLRILLNKAALRKAHTS..........NFRYGKPVQSQVQLKPRDLC 43
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              830525 seqs, 258052604 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                  OM protein - protein search, using sw model
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QR11A8

QR11A6

QC3786

QS1AV6

QS1AV6

QSYMSS

QSYMSS

QSYMSS

QSC35

QSLM3

QSC35

QSC37

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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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Gapop 10.0 , Gapext 0.5
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1: sp_archea:*

2: sp_bacteria:*

3: sp_tungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*
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sp_bacteriap:*
sp_archeap:*
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sp_organelle:*
sp_phage:*
sp_plant:*
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217
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Match Length DB
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Perfect score:
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QBirhl drosophila QBirhl drosophila QBirhl drosophila QBG464 synechococc Q45965 coxiella bu Q9v4j5 drosophila QB109 oryza sativ Q9z64 yersinia pe QBG05 yersinia pe QBR065 yersinia pe QBR065 yersinia pe QBR14 bovine vira QBF18 estendemonas QBF18 estendemonas QBF18 estendemonas QBF18 estendemonas QBF18 estendemonas QBF18 estendemonas QB180 drosophila QB180 drosophila QB180 drosophila QB180 drosophila QB180 drosophila QB181 estendemonalla QB181 estendemonalla QB181 estendemonalla QB231 salmonalla QB271 salmonalla QB271 salmonalla P7454 synechocyst	Vojugo neisseita m Q9vxz7 drosophila
QBIRHO QBIRHI LG QBOGG4 QBIRHI LG QBOGG4 CQ9V4J5 CQ9V4J5 CQ9V4J5 CQ9V4J5 CQ9V4J5 CQ9V4J5 CQ9V4J5 CQ9V4J6 CQ9V4J6 CQ9V4J6 CQ9V4J6 CQ9V7N8 CQ9N7N8 CQ6NGJ6 CQ6NGJ6 CQ6NGJ7 CQ6NG	O9VXZ7
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ALIGNMENTS

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Gaps

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Indels

QBR1A8

RESULT 2

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MEDINE=86106223; PubMed=3943133;

Horwich A.L., Kalousek F., Fenton W.A., Pollock R.A., Rosenberg L.E.;

"Targeting of pre-ornithine transcarbamylase to mitochondria:

definition of critical regions and residues in the leader peptide.";

Cell 44:451-459(1986).

EMBL; M12583; AAA41770.1; -.
                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCPL_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shimogiri T., Koyanagi K., Mannen H., Tsuji S.;
"Ornithine transcarbamylase is expressed in uricotelic animals.";
Bubmitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF134846; AAF61410.1; -.
HSSP; P00480; 10TH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.8%; Score 119; DB 11; Length 41; 66.7%; Pred. No. 2.8e-10; tive 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trachemys scripta elegans.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelec
Testudines; Cryptodira; Testudinoidea; Emydidae; Trachemys.
N.O. — TaxID=31138;
                                                                              1 MLFHLRTLINNAALRNGHNFVVRNFRCGQPLQDKVQLKGRDL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGRRAMS; TIGRO0658; orni carb tr; 1.
PROSITE; PSO0097; CARBANOTLTRANSFERASE; 1.
SEQUENCE 354 AA; 39958 MW; BD6A2C3AEC0F99BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 AA; 4934 MW; 802465955B32374B CRC64;
                                                         1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQLKPRDL
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Last annotation update)
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Last annotation update)
                   10;
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Pred. No. 2.7e-07;
 Pred. No. 7.1e-11;
                                                                                                                                                                                           Ä
                   5; Mismatches
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InterPro; IPR002292; Orn_carbiransf.
InterPro; IPR006131; Offcace_O.
InterPro; IPR006132; OfCace_P.
                                                                                                                                                                                                                                                                                   Ornithine transcarbamylase (Fragment)
                                                                                                                                                                                                                              Created)
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                                                                                                                                                                                       PRT;
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64.3%;
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Pfam; PF02729; OTCace N; 1.
PRINTS; PR00100; AOTCASE.
                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-MAY-2000 (TrEMBLrel. 13,
                   27; Conservative
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Matches 24; Conservative
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                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat)
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Best Local Similarity
 Best Local Similarity
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                   Matches
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Q9IAU8
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Bukaryota, Metacoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae, Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shimogiri T., Koyanagi K., Mannen H., Tsuji S.;
"Ornithine transcarbamylase is expressed in uricotelic animals.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF134841; AAF61405.1; -.
HSSP; P00480; 10TH.
                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75.6%; Score 164; DB 11; Length 351; 83.3%; Pred. No. 5.9e-16; ive 2; Mismatches 5; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 354;
                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (MPR-2002) to the EMBL/GenBank/DDBJ databases.
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InterPro; IPR00229; Orn_carbtransf.
InterPro; IPR006131; OTCace_O.
InterPro; IPR006132; OTCace_P.
Pfam; PF00185; OTCace; 1.
Pfam; PF02729; OTCace; 1.
IIGREAMS; TIGR00659; Orn; 1.
PROSITE; PS00099; CarbaMOYLITRANSFERASE; 1.
SRQUENCE 351 AA; 39365 MW; E6B38BB2FC779F42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MLSNLRILLINNAALRKGHTSVVRHFWCGKPVQSQVQLKGRDL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MLSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQLKPRDL 42
                                                                                                                                    Last sequence update)
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Last annotation update)
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                                                                                                            01-UTN-2002 (TrEMBLrel. 21, Created)
01-UTN-2002 (TrEMBLrel. 21, Last seque
01-WAR-2003 (TrEMBLrel. 23, Last annot
Similar to ornithine transcarbamylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR006130; Asp/orn Cotranf.
InterPro; IPR002292; orn carbtransf.
InterPro; IPR006131; OTCace O.
InterPro; IPR006132; OTCace P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                          PRT;
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HSSP; P00479; 3CSU.
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01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-MAR-2003 (TrEMBLrel. 23,
Ornithine transcarbamylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 83.3
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                            PRELIMINARY;
                                                                                                                                                                                       Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                         TISSUE=Liver;
                                                                                              Q8R1A8;
01-JUN-2002
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7UIN60 RESULT 3 Q9N1U7

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MEDLINE=21332296; PubMed=11427726;
She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
Awayez M.J., Char-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
Thi-Ngoc H.P., Redder F., Schenk M.E., Theriault C., Tolstrup N.,
Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
The complete ganome of the crenarchaeon Sulfolobus solfataricus P2.",
Proc. Natl. Acad. Sci. U.S.A., 98:7835-7840(2001).
        Obermaier B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sulfolobus solfataricus.
Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
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Voukelatou E., Milioni D., Hatzopoulos P., Piravandi E., Oberma. Hilbert H., Duesterhoft A., Moores T., Jones J.D.G., Eneva T., Palme K., Benes V., Rechman S., Ansorge W., Cooke R., Berger C., Delseny M., Voet M., Volckaert G., Mewes H.W., Klosterman S., Schueller C., Chalwatzis N.;
"Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thaliana.";
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0
                                                                                                                                                                                                                                                                                                                                                                   Score 61; DB 10; Length 1286;
Pred. No. 5.8;
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                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                     Hypothetical protein.
SEQUENCE 1286 AA; 143860 MW; F953B283C53D0DEE CRC64;
                                                                                                                                                                                                                       EU Arabidopsis sequencing project;
Submitred (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; 297337; CAB10276.1; -.
EMBL; AL161540; CAB78539.1; -.
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Pfam; PRO824; TGS; 1.

Hypothetical protein; Complete proteome.

SEQUENCE 351 AA; 39916 MW; 046A96BF004865DE CRC64;
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 SNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQ 36
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                                                                                                                                                                                                                                                                                                                                                                     Match 28.1%;
Local Similarity 38.2%;
Wes 13; Conservative
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01-OCT-2001 (TrEMBLrel. 18,
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01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
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                                                                                                                                                         Nature 391:485-488(1998).
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Q9YHY9
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MEDLINE=98121113; PubMed=9461215;
Bevan M., Bant E., Love K., Goodman H., Dean C.,
Bergkamp R., Dirkse W., van Staveren M., Stiekema W., Drost L.,
Bergkamp R., Dirkse W., van Staveren M., Stiekema W., Drost L.,
Ridley P., Hudson S.A., Patel K., Murphy G., Piffannelli P., Wedler H.,
Wedler E., Wambutt R., Weitzenegger T., Pohl T.M., Terryn N.,
Gielen J., Villarroel R., De Clerck R., van Montagu M., Lecharny A.,
Auborg S., Gy I., Kreis M., Lao N., Kavanagh T., Hempel S., Kotter P.,
Entian K.D., Rieger M., Schaeffer M., Punk B., Mueller-Auer S.,
Silvey M., James R., Montfort A., Pons A., Puigdomenech P., Douka A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            core eudicots; Rosidae;
        Gaps
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                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Iguania, Iguanidae, Phrynosomatinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shimogiri T., Koyanagi K., Mannen H., Tsuji S.; "Ornithine transcarbamylase is expressed in uricotelic animals."; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF134844; AAF61408.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MLFNFRSLFSTRNVNKISKHLVQRIRYRHGPPSETPVQLKGRDL 44
        13; Indels
                                                                       1 MLFNLRNLLNAATLRNSSKQLVQHFRSGQPTQTNINLKGRDL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01D49CCB93E4DBD1 CRC64;
                                              1 MLSNLRILLINKAALRKAHTSMVRNFRYGKPVQSQVQLKPRDL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MLSNLRILLNKAALRKAHTSMVRNFRY--GKPVQSQVQLKPRDL
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                                                                     Last annotation update)
                                                                                                                                                                                                                                                             sequence update)
                                                                                                                                                                                                   356 AA.
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        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PROOLOO; ACTCĀSE.
TIGROBAS; OTNI, CALD LT; 1.
PROSITE: POOLOO?; CHRBAMOŸLTRAÑSFERASE; 1.
SEQUENCE 356 AA; 40399 MW; 01D49CCB93E
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InterPro; IPR002292; Orn_Carbtransf.
InterPro; IPR006131; OTCace_O.
InterPro; IPR006132; OTCace_P.
                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                 Last
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      7;
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01-OCT-2000 (TrEMBLrel. 15,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00185; OTCace; 1. Pfam; PF02729; OTCace_N; 1.
                                                                                                                                                                                                                                                                                                       Ornithine transcarbamylase.
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      Conservative
                                                                                                                                                                                                 PRELIMINARY;
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Best Local Similarity
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        22;
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      Matches
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Query Match
Best Local Similarity
Matches 13; Conserv
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01-OCT-2000
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01-MAR-2003
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                                                                                                                                                                                                                                                                       Q9LMN3;
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                                                                                                                                                                                                        RESULT 11
Q9LMN3
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044679
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                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                            SEQUENCE FROM N.A.

STRAIN=BREED WHITE LEGHORN; TISSUE=Kidney;
MEDLINE=99011321; PubMed=979220;
Shimogiri T., Kono M., Mannen H., Mizutani M., Tsuji S.;
Schimogiri T., Kono M., Mannen H., Mizutani M., Tsuji S.;
"Chicken ornithine transcarbamylase gene, structure, regulation, and chromosomal assignment: repetitive sequence motif in intron 3 regulates this enzyme activity.";
J. Blochem. 124:962-974 [1998].

BMEJ, AF065629; AAD12234.1;
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"Comparative genetics of capsular polysaccharide biosynthesis in
Streptococcus pneumoniae types belonging to serogroup 19.",
J. Bacteriol. 181:555-5364 (1999).
EMBL, AF105116, AAD19925.1;
InterPro; IRR001296; Glyco_trans_1.
Perm; PR00534; Glycos_trans_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pneumoniae.
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40245 MW; 20447180BAD9D4ED CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                         Ornithine transcarbamylase precursor (EC 2.1.3.3)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGRFAME; TIGRO0658; orni carb tr; 1.
PROSITE; PS00097; CARBAMOVLITRANSFERASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                  AF065630; AAD33083.1; JOINED.
AF065631; AAD33083.1; JOINED.
AF065632; AAD33083.1; JOINED.
AF065634; AAD33083.1; JOINED.
AF065635; AAD33083.1; JOINED.
AF065636; AAD33083.1; JOINED.
AF065636; AAD33083.1; JOINED.
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InterPro; IPR006130; Asp/Orn Cotranf.
InterPro; IPR00130; Orn_carbtransf.
InterPro; IPR006131; OrGace O.
InterPro; IPR006132; OrCace_P.
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les 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                      AF065638; AAD33083.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTCace N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0100; ACTCASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                               Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00185; OTCace;
Pfam; PF02729; OTCace_N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        354 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         369 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1313;
                                                                                                                                             NCBI TaxID=9031;
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EMBL;
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EMBL;
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Matches
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EMBL;
EMBL;
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                                                    Gaps
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STRAIN=cv. Columbia;
Liu S.X., Sakano H., Yu G., Etgu P., Lee J.M., Lenz C., Pham P.,
Liu S.X., Sakano H., Chin C., Choi E., Chung M.,
Toriumi M., Byun E., Chan A., Chin C., Choi E., Chung M.,
Goldsmith A., Gonzalez A., Liu A., Smith A., Vaysberg M., Altafi H.,
Brooks S., Buehher E., Chao Q., Conn L., Conway A.B., Hansen N.F.,
Johnson-Hoppon C., Khan S., Kim C., Lam B., Miranda M., Nguyen M.,
Federspiel N.A., Theologis A.;
The sequence of BAC Fleft from Arabidopsis thaliana chromosome 1.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
BNBL, AGO36104; AAF813641; -.
SEQUENCE 454 AA; 50928 MW; 70BCZACCG9DEBDCF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosid
eurosids II; Brassicales, Brassicaceae, Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 10; Length 454;
  Length 369;
                                                    Indels
                                                                                                     43
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                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                48 NVHKVLVRLGIKKSDMSMT----YIKYAENQVHLSPEDVC
                                                 14;
                                                                                                     4 NLRILLINKAALRKAHTSMVRNFRYGKPVQSQVQLKPRDLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11;
     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KAAYSRISTDSPSRNYRESQPMGSPVQARPR 452
25.8%; Score 56; DB 2
32.5%; Pred. No. 8.1;
live 9; Mismatches
                                                                                                                                                                                                                                                                                  454 AA
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STRAIN=Bristol N2;
David M., Wohldmann P., Bauer C., Antoniou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.6%; Score 55.5; 45.2%; Pred. No. 12
                                                                                                                                                                                                                                                                                                                                                                                                  F16F4.13 protein.
F16F4.13.
Arabidopsis thaliana (Mouse-ear cress).
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                                                                                                                                                                                                                                                                               PRT;
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MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical 33.8 kDa protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 06, TrEMBLrel. 06, (TrEMBLrel. 23,
                                                    13; Conservative
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us-08-765-244-22.rspt

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compressed between duplicated and and Ddc.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JON-2001 (TrEMBLrel. 17, Last annotation update)
01-JON-2001 (TrEMBLrel. 17, Last annotation update)
01-JON-2001 (TrEMBLrel. 17, Last annotation update)
CG10561 OR ANON-37CS OR CS.
Drosophila lebanonensis (Fruit fly) (Scaptodrosophila lebanonensis)
Bukaryota, Matazoa, Arthropoda, Haxapoda; Insecta, Pterygota;
Bupydroidea; Drosophilidae; Scaptodrosophila,
NCSD_TAXID=7225;
                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
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                                                                                                                                                                                                                                                                                                           Length 300;
                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Klein S., Strausberg R.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC041284, AAH1284.1; -.
Hypothetical protein
SEQUENCE 457 AA; 51021 MW; EE44FE225DD0039B CRC64;
                                                                                                                                                              Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF039051; AAB94269.1; -. wormPep; C14C6.13; EX08168. Hypothetical protein. SEQUENCE 300 AA; 33753 MW; 227DF298FFD8AC83 CRC64;
"The sequence of C. elegans cosmid C14C6.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to hypothetical protein MGC11993.
Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                         14;
                                                                                                                                                                                                                                                                                                                                                                                                                           199 LDNIRELCGQSALQKCSFTRDPNTGFYRPINSEIQ 233
                                                                                                                                                                                                                                                                                                                                                                                                  2 LSNLRILLNKAALRKAHTSMVRNFRYGKPVQSQVQ 36
                                                                                                                                                                                                                                                                                                           Query Match
24.9%; Score 54; DB 5;
Best Local Similarity 31.4%; Pred. No. 13;
Matches 11; Conservative 10; Mismatches 1.
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                                                                                                                                     "Direct Submission.";
                                                                                            STRAIN=Bristol N2;
Waterston R.;
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                                                                      SEQUENCE FROM N.A
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096570
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Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
                                                                                                                                                                                                                                                                                   Query Match 24.9%; Score 54; DB 5; Length 544; Best Local Similarity 34.2%; Pred. No. 25; Matches 13; Conservative 5; Mismatches 20; Indels
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Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 LSNLRILLINKAALRKAHTSMVRNF-RYGK----PVQSQVQLKPRD 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schulz C., Perezgasga L., Fuller M.T.,
"Functional analysis of a Drosophila puromycin-sensitive aminopeptidase gene.",
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF327435, AAC48733.1,
Gene 231:111-120(1999).
-!- FUNCTION: HAS A NONVITAL FUNCTION (BY SIMILARITY).
-!- SUBCELLUIAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
EMBL; AF091239; AAC67584.1; -.
FlyBase; FEGN0025668; Dleb\CG10561.
InterPro; IRR002937; Amino oxidase.
InterPro; IRR002097; Amino oxidase.
InterPro; IRR00293; Amino oxidase; J.
SEQUENCE 544 AA; 61026 MW; CF003E2CBB7D6DBE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             866 AA; 99450 MW; 907F7D14404760AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                               332 VLKNFSAILFKPALPLEKLQAIRNLGYGNÞVKIYLAYK 369
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InterPro; IPR001930, Ala peptase.
InterPro; IPR002014; HPT_SerP_site.
InterPro; IPR002014; HPT_SerP_site.
Pfan; Pr01433; Peptidase M1; 1.
PR017ES; PR00756; ALADIPTÄSE.
PROSITE; PR00142; ZING_PRGERASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Puromycin-sensitive aminopeptidase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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SEQUENCE 866
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